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1631194 0.3219004 t-complex-associated-testis-expressed 1-like 1

366834 0.3217743 envoplakin

839580 0.3216628 ESTs

245485 0.3215041 hypothetical protein MGC5178

815501 0.3214849 hypothetical protein MGC2721

2017403 0.3211799 regulator of G-protein signalling 3

281476 0.3210873 aspartylglucosaminidase

130835 0.3209345 Homo sapiens, Similar to clone FLB3816, clone
IMAGE:3454380, mRNA

77533 0.3205713 inositol polyphosphate-5-phosphatase, 40kD

42076 0.3194462 TRK-fused gene

810998 0.3179036 DKFZP434C131 protein

75859 -1.8328232 N-myc downstream-regulated gene 2

760299 -1.7010462 dickkopf (Xenopus laevis) homolog 3

344720 -1.5196431 glycophorin C (Gerbich blood group)

345670 -1.4445337 ESTs, Moderately similar to I59348 CCAAT binding
transcription factor CBF subunit C - rat [R.norvegicus]

200814 -1.4325283 membrane metallo-endopeptidase (neutral endopeptidase,
enkephalinase, CALLA, CD10)

1882697 -1.4318896 peanut (Drosophila)-like 2

1161564 -1.3891189 desmuslin

788234 -1.3761312 inhibitor of DNA binding 4, dominant negative helix-loop-helix
protein

1558675 -1.3749762 SRY (sex determining region Y)-box 10

285377 -1.3699153 pellino (Drosophila) homolog 2

45099 -1.3515907 regucalcin (senescence marker protein-30)

611532 -1.3158379 troponin I, skeletal, fast

377275 -1.3102234 ataxia-telangiectasia group D-associated protein

810002 -1.3038896 Homo sapiens, clone MGC:19762 IMAGE:3636045, mRNA,
complete cds

1569187 -1.2971252 heparan sulfate (glucosamine) 3-O-sulfotransferase 4

377461 -1.2798035 caveolin 1, caveolae protein, 22kD

712139 -1.2738321 ADP-ribosylation factor-like 7

742685 -1.272916 disabled (Drosophila) homolog 2 (mitogen-responsive
phosphoprotein)

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811920 -1.2690713 interleukin 11 receptor, alpha
796542 -1.2625621 ets variant gene 5 (ets-related molecule)
486683 -1.2614406 Homo sapiens mRNA; cDNA DKFZp564J0323 (from clone
DKFZp564J0323)

753071 -1.2529315 Homo sapiens cDNA: FLJ22528 fis, clone HRC12825

131839 -1.2372478 folate receptor 1 (adult)
300632 -1.2368481 hypothetical protein FLJ21044 similar to Rbig1

839736 -1.2271618 crystallin, alpha B
813265 -1.2230435 Homo sapiens mRNA; cDNA DKFZp564H1916 (from clone
DKFZp564H1916)

1469377 -1.2127781 lipoma HMGIC fusion partner-like 2
490023 -1.2114805 hypothetical protein MGC2648
298122 -1.1962478 frizzled (Drosophila) homolog 7
72778 -1.1752838 caspase 7, apoptosis-related cysteine protease

160192 -1.1751869 ESTs, Weakly similar to 2004399A chromosomal protein
[H.sapiens]
22917 -1.1590598 Homo sapiens mRNA; cDNA DKFZp761M0111 (from clone
DKFZp761M0111)

877621 -1.1501074 nGAP-like protein
840266 -1.1476896 Homo sapiens cDNA: FLJ22667 fis, clone HSI08385

289760 -1.1390686 ESTs, Highly similar to T00391 hypothetical protein KIAA0612
[H.sapiens]
811848 -1.1350073 hypothetical protein
1556433 -1.1222978 GRO3 oncogene
838478 -1.1175047 neurocalcin delta
1473274 -1.1172693 myosin regulatory light chain 2, smooth muscle isoform

1917449 -1.0894686 serum amyloid A4, constitutive
811088 -1.0851546 ephrin-B3
1554167 -1.0818834 hypothetical protein FLJ14529
67741 -1.0705249 PP2135 protein
2106144 -1.067765 regulated in glioma
2056139 -1.0673271 LIM domain protein
767202 -1.0654145 latent transforming growth factor beta binding protein 2

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345034 -1.0600859 small inducible cytokine subfamily B (Cys-X-Cys), member 14
(BRAK)
666879 -1.0463245 annexin A8
130201 -1.0401997 intercellular adhesion molecule 2
878836 -1.037352 secretory granule, neuroendocrine protein 1 (7B2 protein)

52419 -1.0368509 Friedreich ataxia region gene X123
291478 -1.0212528 runt-related transcription factor 3
781014 -1.0161379 suppression of tumorigenicity 5
132857 -1.0084069 Homo sapiens mRNA; cDNA DKFZp586N1323 (from clone
DKFZp586N1323)

529843 -1.0036824 ESTs, Moderately similar to JC5238 galactosylceramide-like
protein, GCP [H.sapiens]

2504881 -1.000863 signal transducer and activator of transcription 5A

69002 -0.9960916 PPAR(gamma) angiopoietin related protein

841308 -0.9953716 myosin, light polypeptide kinase
488404 -0.9880176 Homo sapiens clone TUA8 Cri-du-chat region mRNA

277571 -0.9841522 KIAA1706 protein
1871116 -0.9821709 Homo sapiens mRNA; cDNA DKFZp434C1714 (from clone
DKFZp434C1714); partial cds

897963 -0.9775616 phosphatidic acid phosphatase type 2A
1584540 -0.9754693 Homo sapiens mRNA; cDNA DKFZp586M2022 (from clone
DKFZp586M2022)

196435 -0.9665947 ESTs
140574 -0.9652218 small inducible cytokine subfamily D (Cys-X3-Cys), member 1
(fractalkine, neurotactin)

740620 -0.96496 tropomyosin 2 (beta)
1473471 -0.9623482 KIAA0194 protein
1635320 -0.9586226 amiloride-sensitive cation channel 2, neuronal

416959 -0.957248 nuclear factor I/B
814798 -0.9559895 aldehyde dehydrogenase 1 family, member A3

823871 -0.9429443 SPARC-like 1 (mast9, hevin)
303109 -0.9414602 purinergic receptor (family A group 5)

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270826 -0.9389651 Homo sapiens cDNA FLJ13329 fis, clone OVARC1001795

360254 -0.9286811 cysteine-rich, angiogenic inducer, 61
66491 -0.9280245 plasmolipin
814316 -0.9276916 ribosomal protein L13
153760 -0.9227865 EphB1
811149 -0.9216006 chromosome 9 open reading frame 3
786069 -0.9203158 beta-site APP-cleaving enzyme
208718 -0.9190244 annexin A1
416676 -0.9140494 pellino (Drosophila) homolog 1
248631 -0.9106505 aminomethyltransferase (glycine cleavage system protein T)

76182 -0.9106484 hypothetical protein DKFZp761F241
756708 -0.910505 potassium intermediate/small conductance calcium-activated
channel, subfamily N, member 4

712401 -0.9068788 phosphoinositide-3-kinase, catalytic, delta polypeptide
625399 -0.9066615 hypothetical protein similar to beta-transducin family

753038 -0.893161 kinesin family member C3
162308 -0.8910356 ESTs
796181 -0.8888496 growth arrest-specific 6
133236 -0.8888316 RNA binding motif protein, X chromosome
415816 -0.8887425 ESTs
323780 -0.8879854 Homo sapiens cDNA FLJ11177 fis, clone PLACE1007402

1493218 -0.884795 hypothetical protein FLJ22297
1636166 -0.8845211 KIAA0668 protein
1856063 -0.8833091 tweety (Drosophila) homolog 1
34093 -0.8800259 EST
2028722 -0.8800075 osteoblast specific factor 2 (fasciclin I-like)
811837 -0.8764231 eukaryotic translation elongation factor 1 alpha 1

628955 -0.8761473 forkhead box O1A (rhabdomyosarcoma)
884462 -0.8743987 Down syndrome critical region gene 1
306798 -0.8718483 NGFI-A binding protein 1 (EGR1 binding protein 1)

882248 -0.8700731 transgelin
770935 -0.8700104 hypothetical protein FLJ13511
41208 -0.865227 bone morphogenetic protein 1
768571 -0.8572018 SRY (sex determining region Y)-box 8

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781017 -0.8526926 early growth response 2 (Krox-20 (Drosophila) homolog)

811837 -0.848137

815737 -0.8444322 ATP synthase, H⁺ transporting, mitochondrial F1 complex,
alpha subunit, isoform 1, cardiac muscle

814826 -0.8443265 ESTs

767164 -0.842198 ESTs, Weakly similar to MUC2_HUMAN MUCIN 2
PRECURSOR [H.sapiens]

71087 -0.8416951 v-maf musculoaponeurotic fibrosarcoma (avian) oncogene
family, protein F

283023 -0.8413949 chemokine (C-X3-C) receptor 1

160609 -0.8405669 ESTs

814443 -0.8385965 hypothetical protein MGC3232

142259 -0.8376566 tumor necrosis factor alpha-inducible cellular protein containing
leucine zipper domains; Huntingtin interacting protein L;
transcription factor IIIA-interacting protein

990881 -0.8335353

970590 -0.8333968 Homo sapiens mRNA; cDNA DKFZp434A115 (from clone
DKFZp434A115)

470393 -0.830751 matrix metalloproteinase 7 (matrilysin, uterine)

772913 -0.8306579 calreticulin

741139 -0.8299902 eyes absent (Drosophila) homolog 2

27769 -0.8298821 ESTs

544639 -0.8275232 ESTs

1587710 -0.8252065 period (Drosophila) homolog 1

757191 -0.8247438 ESTs

80344 -0.8243418 interleukin 7 receptor

1635062 -0.8243024 DKFZP586A011 protein

119290 -0.8224756 cortic al thymocyte receptor (X. laevis CTX) like

161456 -0.8215502 serum amyloid A1

1909935 -0.8169271 ESTs

1257131 -0.8163443 ESTs

868396 -0.808677 tyrosine 3-monooxygenase/tryptophan 5-monooxygenase
activation protein, eta polypeptide

1609665 -0.8086161 BarH-like homeobox 2

2016775 -0.8063264 G protein-coupled receptor, family C, group 5, member B

796475	-0.8041136	four and a half LIM domains 3
1555924	-0.8025163	CSR1 protein
416434	-0.8006527	SCN Circadian Oscillatory Protein (SCOP)
322561	-0.7970805	ribosomal protein L31
132711	-0.7962294	Kruppel-like factor 5 (intestinal)
70245	-0.795375	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 50374
283124	-0.7933772	ESTs, Moderately similar to LONG-CHAIN FATTY ACID TRANSPORT PROTEIN [M.musculus]
281190	-0.7927001	ESTs
250883	-0.7925068	ubiquitin-activating enzyme E1-like
346545	-0.7887371	laminin, beta 1
1878409	-0.7869766	catechol-O-methyltransferase
530958	-0.7809384	smoothened (Drosophila) homolog
40027	-0.7779473	ESTs
788136	-0.7778375	phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)- homolog phosphodiesterase E4)
1626304	-0.7769866	spinal cord-derived growth factor-B
1474337	-0.7766266	phosphorylase, glycogen; brain
85840	-0.7754435	nicotinamide N-methyltransferase
290378	-0.7751825	podocalyxin-like
2243051	-0.7736287	kallikrein 8 (neuropsin/ovasin)
813256	-0.7731864	ATP-binding cassette, sub-family B (MDR/TAP), member 1
47043	-0.7729643	tensin
343695	-0.7706809	hypothetical protein FLJ10875
491403	-0.7700599	tumor necrosis factor receptor superfamily, member 1B
767765	-0.7691523	GTP-binding protein overexpressed in skeletal muscle
681992	-0.7691299	Homo sapiens cDNA FLJ13384 fis, clone PLACE1001062, highly similar to Homo sapiens mRNA for lysine-ketoglutarate reductase/saccharopine dehydrogenase
505864	-0.7677235	RaIGDS-like gene
139660	-0.7677153	ESTs
869450	-0.7659922	ribosomal protein L11
162308	-0.7654139	
209537	-0.763749	zinc finger protein 221
753162	-0.7617972	KIAA0603 gene product

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810728 -0.7607171 hypothetical gene ZD52F10
366591 -0.7595643 T-cell lymphoma invasion and metastasis 2

488258 -0.7574184 collagen, type XVI, alpha 1
32489 -0.7571259 hypothetical protein DKFZp566A1524
1519147 -0.7548183
418159 -0.7545888 synaptogyrin 1
80727 -0.7538606 receptor tyrosine kinase-like orphan receptor 1

593023 -0.7516846 dystrobrevin, beta
586803 -0.7423407 placental growth factor, vascular endothelial growth factor-
related protein
188335 -0.7399294 egf-like module containing, mucin-like, hormone receptor-like
sequence 2
1161775 -0.7380353 villin 1
490668 -0.7364434 Homo sapiens mRNA; cDNA DKFZp586B211 (from clone
DKFZp586B211)

1474900 -0.736252 keratin 15
378813 -0.7346408 secretory leukocyte protease inhibitor (antileukoproteinase)

1630990 -0.7312981 ribosomal protein L29
280907 -0.7307519 Kruppel-type zinc finger protein
742562 -0.730047 chromosome 16 open reading frame 5
73252 -0.7283898 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)

26566 -0.7278186 protein-O-mannosyltransferase 1
1471829 -0.7275378 uncharacterized hypothalamus protein HSMNP1

289428 -0.7270494 neurotrophic tyrosine kinase, receptor, type 2

898092 -0.7267434 connective tissue growth factor
34150 -0.7263513 ESTs
24958 -0.7225195 Homo sapiens mRNA; cDNA DKFZp434C2016 (from clone
DKFZp434C2016)

725680 -0.7197488 transcription factor AP-2 gamma (activating enhancer-binding
protein 2 gamma)

77972 -0.7194713 complement component 3
1686766 -0.7192745 Rag D protein
471196 -0.7192268 integral membrane protein 3

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431231 -0.7182897 EGF-containing fibulin-like extracellular matrix protein 2
1908834 -0.7177051 ubiquitin A-52 residue ribosomal protein fusion product 1
207735 -0.7167416 serine (or cysteine) proteinase inhibitor, clade A (alpha-1
antiproteinase, antitrypsin), member 1
754157 -0.7165332 Homo sapiens mRNA; cDNA DKFZp434K2172 (from clone
DKFZp434K2172)
35828 -0.7163689 diphtheria toxin receptor (heparin-binding epidermal growth
factor-like growth factor)
1946448 -0.7150027 caveolin 2
470148 -0.712917 ESTs
840944 -0.7099353 early growth response 1
809784 -0.7095414 kallikrein 6 (neurosin, zyme)
877827 -0.7093855 ribosomal protein S27a
32493 -0.7093777 integrin, alpha 6
813520 -0.7092422 EphB3
782501 -0.7086066 hypothetical protein PP1665
27544 -0.708383 prominin (mouse)-like 1
184022 -0.7070266 amyloid beta (A4) precursor protein-binding, family B, member
1 (Fe65)
323238 -0.7042807 GRO1 oncogene (melanoma growth stimulating activity, alpha)
488956 -0.70192 CUG triplet repeat, RNA-binding protein 2
1926246 -0.701769 ESTs, Moderately similar to T46371 hypothetical protein
DKFZp434P1018.1 [H.sapiens]
325365 -0.7012106 HIV-1 rev binding protein 2
221846 -0.6982802 checkpoint suppressor 1
1870305 -0.6958213 heat shock 27kD protein 2
277044 -0.6947855 KIAA1183 protein
503335 -0.6944661 hypothetical protein FLJ11196
757873 -0.6940266 cyclin-dependent kinase 5, regulatory subunit 1 (p35)
2306682 -0.6934667 A kinase (PRKA) anchor protein (yotiao) 9
1864302 -0.6932327 E74-like factor 5 (ets domain transcription factor)
843070 -0.6925728 nucleoporin 88kD
812975 -0.6921755 KIAA0172 protein

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46129 -0.6919169 ESTs, Highly similar to T17245 hypothetical protein
DKFZp586J0917.1 [H.sapiens]

270917 -0.6918383 secreted frizzled-related protein 1
789382 -0.6898974 Notch (Drosophila) homolog 4
611481 -0.6894079 HMG-box transcription factor TCF-3
35300 -0.688788 KIAA0869 protein
50892 -0.6887497 Homo sapiens, clone MGC:9913 IMAGE:3870821, mRNA,
complete cds
366100 -0.6885372 matrilin 2
345056 -0.6863529 KIAA1404 protein
2783721 -0.6854649 cholinergic receptor, nicotinic, beta polypeptide 1 (muscle)

178137 -0.6839022 ribosomal protein L34
1626996 -0.682449 c-fos induced growth factor (vascular endothelial growth factor
D)
188388 -0.6824191 integrin, alpha 10
133518 -0.6817662 microtubule-associated protein, RP/EB family, member 2

839796 -0.6807912 candidate tumor suppressor p33 ING1 homolog

726582 -0.6807781 actin-related protein 3-beta
50586 -0.6794282 KIAA1545 protein
491763 -0.679034 interleukin 1, beta
52096 -0.6789228 platelet-derived growth factor receptor, alpha polypeptide

263716 -0.6767498 collagen, type VI, alpha 1
2095066 -0.676021 alcohol dehydrogenase 1C (class I), gamma polypeptide

1475738 -0.6753091 ribosomal protein S25
41869 -0.6747514 hypothetical protein FLJ11017
1350439 -0.6740833 KIAA0015 gene product
502689 -0.6739476 Homo sapiens clone HH409 unknown mRNA

773373 -0.6730112 hypothetical protein MGC14258
308539 -0.6726187 Homo sapiens cDNA FLJ12777 fis, clone NT2RP2001720

343760 -0.6724144 SH3 domain binding glutamic acid-rich protein like 2

769959 -0.6720196 collagen, type IV, alpha 2
2252954 -0.6687686 enhancer of filamentation 1 (cas-like docking; Crk-associated
substrate related)

70201 -0.6675012 mitochondrial solute carrier

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505243 -0.6671218 inositol 1,4,5-triphosphate receptor, type 2
897731 -0.6670507 latrophilin
296880 -0.6655878 membrane protein, palmitoylated 1 (55kD)
1486082 -0.6635259 heparin-binding growth factor binding protein

1470278 -0.6633411 hypothetical protein FLJ21841
177665 -0.6624986
725152 -0.6591675 hypothetical protein DKFZp762A227
247616 -0.6585351 lipoma HMGIC fusion partner
752668 -0.65723 KIAA0440 protein
837870 -0.657186 proline arginine-rich end leucine-rich repeat protein

744918 -0.6552361 Homo sapiens mRNA; cDNA DKFZp761I0911 (from clone
DKFZp761I0911)

39600 -0.6540275 adenylate kinase 5
795288 -0.6528792 ubiquitin specific protease 4 (proto-oncogene)

1665444 -0.651994 tumor endothelial marker 1 precursor
774078 -0.6508021 leiomodulin 1 (smooth muscle)
415233 -0.6506593 ribosomal protein L37a
307029 -0.6500872 ribosomal protein L26
78946 -0.648366 Homo sapiens pyruvate dehydrogenase kinase 4 mRNA, 3'
untranslated region, partial sequence

785733 -0.6476493 hypothetical protein FLJ12892
415415 -0.646492 EST, Moderately similar to RL1X_HUMAN 60S RIBOSOMAL
PROTEIN L18A [H.sapiens]

858167 -0.6453859 fatty-acid-Coenzyme A ligase, long-chain 4

823714 -0.642903 nuclear receptor co-repressor/HDAC3 complex subunit

193913 -0.6425581 v-src-1 Yamaguchi sarcoma viral related oncogene homolog

220395 -0.6418175 hypothetical protein FLJ23293 similar to ARL-6 interacting
protein-2
840942 -0.6383764 major histocompatibility complex, class II, DP beta 1

725308 -0.6371261 ras inhibitor
1492147 -0.636656 ribosomal protein S4, X-linked
1466893 -0.6364598 ESTs
75078 -0.6362307 ESTs

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796152 -0.6356106 Homo sapiens cDNA FLJ11685 fis, clone HEMBA1004934
190059 -0.634814 guanine nucleotide binding protein (G protein), gamma 7
840511 -0.6341661 vimentin
81409 -0.6338327 GABA(A) receptor-associated protein like 1
745490 -0.6329354 hypothetical protein FLJ20607
530036 -0.6324794 hypothetical protein FLJ13078
755855 -0.6298333 solute carrier family 25 (mitochondrial carrier; adenine
nucleotide translocator), member 6
785538 -0.6289951 Homo sapiens mRNA; cDNA DKFZp434N2116 (from clone
DKFZp434N2116)
2284803 -0.6265431 secretory carrier membrane protein 1
1623016 -0.6263561 EST
154472 -0.6253276 fibroblast growth factor receptor 1 (fms-related tyrosine kinase
2, Pfeiffer syndrome)
774754 -0.6243946 catenin (cadherin-associated protein), beta 1 (88kD)
1572298 -0.6228686 CD3Z antigen, zeta polypeptide (TiT3 complex)
2252417 -0.6222381 ribosomal protein S10
180803 -0.621787 inositol polyphosphate-1-phosphatase
683059 -0.6216483 Cdc42 effector protein 3
1577736 -0.6215965 epidermal growth factor (beta-urogastrone)
241489 -0.6212938 adrenergic, beta-2-, receptor, surface
2316441 -0.6206597 ras homolog gene family, member C
1712825 -0.6204409 ESTs
52724 -0.6199204 hypothetical protein FLJ20241
150897 -0.6188264 UDP-GlcNAc:betaGal beta-1,3-N-
acetylglucosaminyltransferase 3
823851 -0.6182341 AE-binding protein 1
810057 -0.6178096 vasoactive intestinal peptide receptor 1
81316 -0.6176265 ESTs
298134 -0.6152731 frizzled (Drosophila) homolog 1
2028238 -0.6141182 KIAA0300 protein
1898758 -0.6126872 BCE-1 protein
250797 -0.6124667 hypothetical protein FLJ20038
754040 -0.610807 NS1-associated protein 1
1584628 -0.6102937 alpha-actinin-2-associated LIM protein

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230910 -0.6096107
172783 -0.6088873 hypothetical protein FLJ10390
824799 -0.6054867 ART-4 protein
785967 -0.6049171 erythrocyte membrane protein band 4.1-like 2

342349 -0.603487 mitogen-activated protein kinase kinase kinase 14

67067 -0.6003961 Homo sapiens mRNA; cDNA DKFZp564O222 (from clone
DKFZp564O222)

1533710 -0.5988282 ortholog of mouse integral membrane glycoprotein LIG-1

768007 -0.5983563 hypothetical protein
1707637 -0.5964339 ESTs
1634832 -0.5931096 class I cytokine receptor
1609625 -0.5920312 selectin P ligand
1592530 -0.5918818 mammalian inositol hexakisphosphate kinase 2

272706 -0.5914377 alpha2,3-sialyltransferase
897720 -0.5904719 trophinin
1472735 -0.5888169 metallothionein 1E (functional)
767641 -0.5881449 mitogen-activated protein kinase 8 interacting protein 2

1651906 -0.5863631 hypothetical protein FLJ23544
564801 -0.5824549 Homo sapiens cDNA: FLJ21409 fis, clone COL03924

248886 -0.5823315 rab3 GTPase-activating protein, non-catalytic subunit (150kD)

250654 -0.5815576 secreted protein, acidic, cysteine-rich (osteonectin)

1968422 -0.5802058 Homo sapiens mRNA full length insert cDNA clone
EUROIMAGE 1968422
712829 -0.5797871 LIM domain only 2 (rhombotin-like 1)
752837 -0.5794612 Homo sapiens mRNA for FLJ00074 protein, partial cds

346902 -0.5794362 ESTs, Weakly similar to ALU2_HUMAN ALU SUBFAMILY SB
SEQUENCE CONTAMINATION WARNING ENTRY
[H.sapiens]

782193 -0.5788147 thioredoxin
358531 -0.5784457 v-jun avian sarcoma virus 17 oncogene homolog

2271240 -0.5782432 hypothetical protein

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66532 -0.5773248 endothelin 3
120106 -0.5770131 caspase 1, apoptosis-related cysteine protease (interleukin 1,
beta, convertase)
810552 -0.5768989 B-cell associated protein
770848 -0.5767154 ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J
SEQUENCE CONTAMINATION WARNING ENTRY
[H.sapiens]
1032831 -0.5764161 glycosyltransferase
460403 -0.5739604 laminin, gamma 2 (nicein (100kD), kalinin (105kD), BM600
(100kD), Herlitz junctional epidermolysis bullosa))
489755 -0.5730453 a disintegrin and metalloproteinase domain 12 (meltrin alpha)
502753 -0.5724623 angiopoietin 2
68534 -0.5724394 Homo sapiens cDNA: FLJ22290 fis, clone HRC04405
854645 -0.5723062 CDC-like kinase 3
322024 -0.5714933 ESTs, Highly similar to T12495 hypothetical protein
DKFZp434H071.1 [H.sapiens]
140071 -0.5708303 frizzled-related protein
788518 -0.5697316 peroxisomal membrane protein 3 (35kD, Zellweger syndrome)
240752 -0.56913 hypothetical protein MGC14797
773487 -0.5686324 hypothetical protein MGC3032
1404774 -0.5685596 parathyroid hormone-like hormone
814815 -0.5675649 plakophilin 4
462939 -0.5662456 ESTs
240248 -0.5660209 transferrin
208001 -0.5640857 CD59 antigen p18-20 (antigen identified by monoclonal
antibodies 16.3A5, EJ16, EJ30, EL32 and G344)
1909433 -0.5638242 DKFZP727C091 protein
1636360 -0.5629882 hypothetical protein FLJ14957
138242 -0.5621088 ESTs, Moderately similar to MAS2_HUMAN MANNAN-
BINDING LECTIN SERINE PROTEASE 2 PRECURSOR
[H.sapiens]
703964 -0.5620699 inositol polyphosphate phosphatase-like 1
1522734 -0.5618289 ESTs
843094 -0.5617478 ubiquitin-like 1 (sentrin)

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491519 -0.561401 Homo sapiens clone 24775 mRNA sequence

377314 -0.561312 casein kinase 2, alpha prime polypeptide

208969 -0.561267 EST

788558 -0.5600825 KIAA1479 protein

785530 -0.5600048 integrin, alpha 1

1473131 -0.5594101 transducin-like enhancer of split 2, homolog of Drosophila
E(sp1)

812959 -0.5591846 KIAA1638 protein

868169 -0.5584677 lipoprotein lipase

322233 -0.5578912 ribosomal protein, large, P0

50519 -0.5577761 aryl hydrocarbon receptor nuclear translocator-like

299720 -0.5565137

215000 -0.555725 vasoactive intestinal peptide receptor 1

51981 -0.5554908 ribosomal protein L7a

703541 -0.5534921 KIAA1858 protein

238907 -0.5534598 hypothetical protein, clone
Telethon(Italy_B41)_Strait02270_FL142

415613 -0.5528761 DHHC1 protein

282404 -0.5528532 Homo sapiens mRNA for KIAA1671 protein, partial cds

344588 -0.55146 kallikrein 5

746373 -0.5513143 RNA polymerase I transcription factor RRN3

491186 -0.5507413 Homo sapiens cDNA: FLJ23131 fis, clone LNG08502

75059 -0.5504962 poly(A)-binding protein, cytoplasmic 1-like

345764 -0.5504113 special AT-rich sequence binding protein 1 (binds to nuclear
matrix/scaffold-associating DNA's)

1577920 -0.5496944 ESTs

288748 -0.5493871 Homo sapiens, clone MGC:5352 IMAGE:3048106, mRNA,
complete cds

810097 -0.5487174 Homo sapiens cDNA: FLJ21721 fis, clone COLF0381

755881 -0.5473964 aquaporin 5

1568391 -0.5467858 plastin 3 (T isoform)

290866 -0.5467613 v-raf-1 murine leukemia viral oncogene homolog 1

503671 -0.5461871 Homo sapiens cDNA FLJ14368 fis, clone HEMBA1001122

2388571 -0.5459823 A kinase (PRKA) anchor protein 8

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811779 -0.5291718 phosphoinositide-3-kinase, regulatory subunit, polypeptide 1
(p85 alpha)
488130 -0.5289721 Homo sapiens cDNA FLJ20767 fis, clone COL06986
299720 -0.5284407
159462 -0.528299 serum constituent protein
1570427 -0.5280955 hypothetical protein MGC4309
2308346 -0.5268833 cyclin-dependent kinase 2
1881774 -0.5265891 KIAA1678
591055 -0.5258289 protein kinase C and casein kinase substrate in neurons 2
470128 -0.5253542 myosin IE
687990 -0.5253354 Rac/Cdc42 guanine exchange factor (GEF) 6
753620 -0.5248489 insulin-like growth factor binding protein 6
80374 -0.5236475 pyruvate dehydrogenase (lipoamide) alpha 1
878421 -0.5233873 transgelin 2
343079 -0.5224833 Homo sapiens mRNA; cDNA DKFZp761P0114 (from clone
DKFZp761P0114)
284592 -0.5205573 PRO1659 protein
855061 -0.5203046 vascular endothelial growth factor B
183704 -0.5184644 Homo sapiens, clone MGC:13446 IMAGE:4275731, mRNA,
complete cds
155896 -0.5182247 ORF
842939 -0.5172329 adenosine deaminase, RNA-specific, B1 (homolog of rat RED1)
685185 -0.5172158 reticulon 2
753301 -0.5171758 carcinoembryonic antigen-related cell adhesion molecule 1
(biliary glycoprotein)
795178 -0.5169102 lactate dehydrogenase C
1911663 -0.5168962 ESTs
345023 -0.5166203 ESTs, Highly similar to T08701 hypothetical protein
DKFZp564N123.1 [H.sapiens]
1631682 -0.5162406 peptidylprolyl isomerase E (cyclophilin E)
868308 -0.5157133 ribosomal protein S23
809998 -0.5144681 amylase, alpha 2A; pancreatic
771004 -0.5144276 KIAA1201 protein
842896 -0.5137089 hypothetical protein DKFZp762L0311
714213 -0.5129593 tumor necrosis factor receptor superfamily, member 6

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197056 -0.5128128 ESTs
415191 -0.512457 KIAA0161 gene product
2306752 -0.5123647 stathmin-like 2
469306 -0.5113377 gastrin-releasing peptide
824602 -0.5107682 interferon, gamma-inducible protein 16
307687 -0.5106552 protease, serine, 16 (thymus)
1637296 -0.5105214 ribosomal protein S24
1358393 -0.5090372 mitogen-activated protein kinase kinase 3
504940 -0.508056
713839 -0.5080365 transcription factor AP-4 (activating enhancer-binding protein 4)

220293 -0.5078291 Homo sapiens cDNA: FLJ21800 fis, clone HEP00618

125342 -0.5078237 SUMO-1-specific protease
1601845 -0.5074894 Ca2+-promoted Ras inactivator
240620 -0.5065007 vascular Rab-GAP/TBC-containing
43679 -0.5063146 ESTs
825013 -0.505654 acidic protein rich in leucines
2116188 -0.5046972 histone deacetylase 5
161998 -0.5044691 hypothetical protein FLJ23138
83999 -0.5044612 Human DNA sequence from clone 889N15 on chromosome
Xq22.1-22.3. Contains part of the gene for a novel protein
similar to X. laevis Cortical Thymocyte Marker CTX, the
possibly alternatively spliced gene for 26S Proteasome subunit
p28 (Ankyrin repeat prote

593840 -0.5033966 DKFZP564K1964 protein
51448 -0.5031992 activating transcription factor 3
383501 -0.502319 regulator of G-protein signalling 9
2018423 -0.501705 death-associated protein kinase 2
796984 -0.5010588 cytochrome b-245, beta polypeptide (chronic granulomatous
disease)
1160723 -0.5005952 LIM domain kinase 2
414999 -0.5002542 ets variant gene 4 (E1A enhancer-binding protein, E1AF)

770212 -0.4981295 chitinase 3-like 1 (cartilage glycoprotein-39)

48518 -0.4966991 ATP-binding cassette, sub-family A (ABC1), member 5

85634 -0.4961026 complement component 1, s subcomponent

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341763 -0.4953701 caspase 5, apoptosis-related cysteine protease

812161 -0.4948424 ESTs

1417886 -0.4941304 hypothetical protein FLJ23239

1500815 -0.4934665 Homo sapiens cDNA: FLJ22130 fis, clone HEP19632

868400 -0.4928479 glutaminyl-tRNA synthetase

809894 -0.491862 acetyl-CoA synthetase

753745 -0.4917192 ESTs, Weakly similar to S57447 HPBR11-7 protein [H.sapiens]

85394 -0.4913773 phosphatidic acid phosphatase type 2B

134192 -0.4908497 ESTs

813698 -0.4898644 sprouty (Drosophila) homolog 2

253884 -0.4897811 Human BAC clone GS1-99H8

131012 -0.4897744 hypothetical protein FLJ10633

855755 -0.4897236 fibrillarin

1711456 -0.4896574 H factor (complement)-like 1

815142 -0.4881454 spastic ataxia of Charlevoix-Saguenay (sacsin)

2413337 -0.4879268 sortilin-related receptor, L(DLR class) A repeats-containing

327432 -0.4870045 semaphorin Y

1897944 -0.4855156 ESTs, Weakly similar to T00366 hypothetical protein KIAA0669 [H.sapiens]

Example VI: Genes for discriminating between normal and ADH (non-malignant) versus DCIS and IDC (malignant)

As shown in Table 5 below, 400 genes were identified as being able to discriminate between normal and ADH (non-malignant) versus DCIS and IDC (malignant).

Table 5

CloneID	Weight	Description
796469	1.4207633	HSPC150 protein similar to ubiquitin-conjugating enzyme
488964	1.3447179	H2A histone family, member O

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1505038	1.3277637	hypothetical protein FLJ20171
1500000	1.2926116	H2B histone family, member B
1554549	1.2787033	hydroxyacyl glutathione hydrolase
812238	1.2664748	hypothetical protein MGC4692
35147	1.2581066	ESTs, Weakly similar to unnamed protein product [H.sapiens]
122077	1.2576139	putative membrane protein
788654	1.2573483	growth factor receptor-bound protein 2
595037	1.2486446	retinoic acid induced 3
565319	1.2155833	Homo sapiens mRNA; cDNA DKFZp564B1264 (from clone DKFZp564B1264)
283919	1.2112507	H2A histone family, member L
1917941	1.1872008	purine-rich element binding protein B
359887	1.1837896	translocase of inner mitochondrial membrane 17 (yeast) homolog A
471568	1.1673113	hematological and neurological expressed 1
290841	1.1670252	H2B histone family, member A
796694	1.1580364	baculoviral IAP repeat-containing 5 (survivin)
366132	1.1440486	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD
823598	1.1425746	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12
1323448	1.1309009	cysteine-rich protein 1 (intestinal)
810711	1.1074523	stearoyl-CoA desaturase (delta-9-desaturase)
741474	1.0870449	glucose phosphate isomerase
745606	1.0663136	hypothetical protein PP591
2054635	1.0613961	proteasome (prosome, macropain) subunit, alpha type, 7
178805	1.0513873	Human DNA sequence from clone RP5-850E9 on chromosome 20. Contains part of the gene for a novel C2H2 type zinc finger protein similar to Drosophila Scratch (Scrt), Slug and Xenopus Snail, a novel gene similar to Drosophila CG6762, STSs, GSSs and five CpG
347373	1.0454939	transcription elongation factor B (SIII), polypeptide 1 (15kD, elongin C)

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199403	1.0142329	lectin, galactoside-binding, soluble, 8 (galectin 8)
814054	1.0130821	KIAA0040 gene product
2029173	1.0094499	ESTs, Weakly similar to N-WASP [H.sapiens]
209066	1.0066096	
782428	1.0008279	KIAA0250 gene product
769921	0.9944462	ubiquitin carrier protein E2-C
470061	0.9920108	seven in absentia (Drosophila) homolog 2
796723	0.9915885	Homo sapiens clone CDABP0014 mRNA sequence
1609836	0.9886168	glutamate-ammonia ligase (glutamine synthase)
2322367	0.9859632	reticulon 4
280375	0.9793036	PRO2000 protein
2016908	0.969649	ESTs, Weakly similar to CA13_HUMAN COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [H.sapiens]
1858892	0.9669022	hypothetical protein MGC4825
46248	0.9628117	ADP-ribosyltransferase (NAD ⁺ ; poly (ADP-ribose) polymerase)
2014034	0.9619198	methylene tetrahydrofolate dehydrogenase (NAD ⁺ dependent), methenyltetrahydrofolate cyclohydrolase
898032	0.9547022	KIAA0097 gene product
725454	0.9476507	CDC28 protein kinase 2
79520	0.9457391	RAB2, member RAS oncogene family
810558	0.943041	proteasome (prosome, macropain) 26S subunit, ATPase, 4
272529	0.9423688	phosphomannomutase 2
122241	0.939204	proteasome (prosome, macropain) subunit, beta type, 2
469686	0.9381847	Ric (Drosophila)-like, expressed in many tissues
624667	0.9336899	CGI-92 protein
488202	0.932881	ESTs, Weakly similar to YZ28_HUMAN HYPOTHETICAL PROTEIN ZAP128 [H.sapiens]
825470	0.9274271	topoisomerase (DNA) II alpha (170kD)
1640821	0.920874	ESTs, Weakly similar to I78885 serine/threonine- specific protein kinase [H.sapiens]

686552	0.9182272	golgi phosphoprotein 1
2016648	0.917373	Homo sapiens mRNA; cDNA DKFZp434N1728 (from clone DKFZp434N1728)
1911343	0.9110591	RAB26, member RAS oncogene family
781097	0.9100493	reticulon 3
244801	0.908481	Rho guanine exchange factor (GEF) 11
754628	0.9061145	ESTs
1574058	0.9058211	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta)
753299	0.9019921	hypothetical protein FLJ10504
811774	0.9014801	CGI-49 protein
595213	0.8978322	hypothetical protein
868128	0.8970146	JM4 protein
810124	0.8891272	platelet-activating factor acetylhydrolase, isoform Ib, gamma subunit (29kD)
66406	0.8888639	hypothetical protein DKFZp762E1312
1636092	0.8841788	hypothetical protein FLJ20657
1869201	0.8825788	hypothetical protein MGC2745
625923	0.8821749	phosphoenolpyruvate carboxykinase 2 (mitochondrial)
1492238	0.8804306	HSPC003 protein
731044	0.8716644	glutaredoxin 2
839682	0.8696528	ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13)
951233	0.8614727	proteasome (prosome, macropain) subunit, beta type, 3
843195	0.8606568	phosphoserine phosphatase
288999	0.8593924	small protein effector 1 of Cdc42
51773	0.8588635	hypothetical protein MGC3077
209066	0.8582298	serine/threonine kinase 15
1474955	0.8573467	TATA box binding protein (TBP)-associated factor, RNA polymerase II, N, 68kD (RNA-binding protein 56)
2043167	0.8551193	BCL2-associated athanogene 3
742707	0.8515067	ESTs, Weakly similar to MUC2_HUMAN MUCIN 2 PRECURSOR [H.sapiens]
743589	0.8514377	ESTs, Weakly similar to T2D3_HUMAN TRANSCRIPTION INITIATION FACTOR TFIID 135 KDA SUBUNIT [H.sapiens]

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704414	0.8498631	small nuclear ribonucleoprotein polypeptides B and B1
2309073	0.8484971	frizzled (Drosophila) homolog 5
2052113	0.8477245	hypothetical protein FLJ10903
686172	0.846207	KIAA0008 gene product
150003	0.8447372	hypothetical protein FLJ13187
705064	0.8401441	transforming, acidic coiled-coil containing protein 3
1709791	0.8397779	BAI1-associated protein 1
1469425	0.8391993	SRY (sex determining region Y)-box 22
429799	0.8386406	hypothetical protein FLJ21939 similar to 5-azacytidine induced gene 2
729975	0.8385313	meningioma expressed antigen 5 (hyaluronidase)
1393018	0.8376676	general transcription factor IIIC, polypeptide 1 (alpha subunit, 220kD)
1492463	0.8360771	selenoprotein X, 1
2028949	0.8358024	hypothetical protein PRO1855
789012	0.8351735	fibulin 2
470124	0.8347241	RAD1 (S. pombe) homolog
1409509	0.8339967	troponin T1, skeletal, slow
1605426	0.8317254	hypothetical protein FLJ13352
44292	0.831599	Homo sapiens mRNA; cDNA DKFZp434C107 (from clone DKFZp434C107)
1435003	0.8311727	tumor suppressing subtransferable candidate 1
503215	0.8286483	pilin-like transcription factor
504308	0.8199799	hypothetical protein FLJ10540
785707	0.8176557	protein regulator of cytokinesis 1
1500162	0.8155519	ESTs
149355	0.8134342	translocating chain-associating membrane protein
1845169	0.8131362	RAB35, member RAS oncogene family
869375	0.808792	isocitrate dehydrogenase 2 (NADP+), mitochondrial
1492426	0.8032542	chromosome 19 open reading frame 3
782513	0.8030042	interferon, alpha-inducible protein (clone IFI-6-16)
813281	0.8016742	WW domain-containing protein 1
814378	0.8015236	serine protease inhibitor, Kunitz type, 2

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700792	0.8005506	cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase)
340558	0.7990715	actin related protein 2/3 complex, subunit 5 (16 kD)
842994	0.7983201	cathepsin Z
138189	0.7953361	Wolfram syndrome 1 (wolframin)
289978	0.7931469	ubiquitin-like 4
2019223	0.7893602	mitochondrial ribosomal protein L17
2110511	0.7863117	artemin
814528	0.7845635	Homo sapiens cDNA: FLJ22139 fis, clone HEP20959
1573251	0.7816689	peroxisomal long-chain acyl-coA thioesterase
773922	0.7799164	KIAA0005 gene product
172517	0.7779159	hippocalcin-like 1
564981	0.7745626	ESTs
1420370	0.7726877	biliverdin reductase B (flavin reductase (NADPH))
308466	0.771216	GTP-binding protein Sara
199645	0.769591	nicastrin
1422338	0.7690604	ribonucleotide reductase M2 polypeptide
1474424	0.7689082	Homo sapiens cDNA FLJ12758 fis, clone NT2RP2001328
813751	0.7665427	sialyltransferase 4C (beta-galactosidase alpha-2,3-sialyltransferase)
131094	0.7626373	Homo sapiens cDNA: FLJ21587 fis, clone COL06946
842980	0.762412	developmentally regulated GTP-binding protein 1
212542	0.7585053	Homo sapiens cDNA FLJ12900 fis, clone NT2RP2004321
108425	0.7581954	
811761	0.7578696	Nijmegen breakage syndrome 1 (nibrin)
241348	0.757138	prenylcysteine lyase
810725	0.7561061	ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) 21kD
1460110	0.7559869	proteasome (prosome, macropain) subunit, beta type, 5
120749	0.7545697	ESTs, Moderately similar to KIAA1215 protein [H.sapiens]
827171	0.7543905	ESTs

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39884	0.7526496	IMP (inosine monophosphate) dehydrogenase 1
124298	0.7507816	microsomal glutathione S-transferase 3
753378	0.7492212	hypothetical protein FLJ22649 similar to signal peptidase SPC22/23
210862	0.7483198	acyl-Coenzyme A oxidase 1, palmitoyl
785766	0.7476331	hypothetical protein
1553306	0.7471557	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11
470099	0.7443747	HT002 protein; hypertension-related calcium- regulated gene
83363	0.7435058	protein-L-isoaspartate (D-aspartate) O- methyltransferase
489351	0.7422879	hypothetical protein DKFZp566J2046
810612	0.7419597	S100 calcium-binding protein A11 (calgizzarin)
825585	0.741258	tubulin-specific chaperone e
1456348	0.7401571	N-acetylneuraminic acid phosphate synthase; sialic acid synthase
1473922	0.7399948	actin related protein 2/3 complex, subunit 3 (21 kD)
150314	0.739762	lysophospholipase I
897806	0.7388301	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)
811585	0.738212	huntingtin (Huntington disease)
685516	0.7378926	putative G protein-coupled receptor
76605	0.7376829	nesca protein
1476053	0.7367106	RAD51 (S. cerevisiae) homolog (E coli RecA homolog)
221295	0.7342275	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein
824879	0.7333071	hypothetical protein MGC11275
768570	0.732628	hypothetical protein FLJ11280
73009	0.731401	ESTs, Weakly similar to A43932 mucin 2 precursor, intestinal [H.sapiens]
564492	0.7301895	mitochondrial carrier homolog 2
2017415	0.7281714	centromere protein A (17kD)
788654	0.7244749	
488505	0.7242619	accessory proteins BAP31/BAP29
824962	0.7238234	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)

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1616253	0.7231756	breast carcinoma amplified sequence 1
1435862	0.723081	antigen identified by monoclonal antibodies 12E7, F21 and O13
786067	0.7228184	cell division cycle 25B
2050827	0.7211304	proteasome (prosome, macropain) 26S subunit, ATPase, 5
248649	0.7210707	hypothetical protein FLJ13910
51532	0.7195798	ADP-ribosylation factor-like 6 interacting protein
727078	0.7184618	Homo sapiens cDNA: FLJ23602 fis, clone LNG15735
37708	0.7163849	hypothetical protein MGC3101
430235	0.7162503	H2B histone family, member Q
897770	0.715754	
292936	0.7154295	hypothetical protein FLJ10468
365738	0.7152855	ESTs
845363	0.714201	non-metastatic cells 1, protein (NM23A) expressed in
809944	0.7139515	KIAA0310 gene product
1631699	0.7115561	valosin-containing protein
813629	0.7102574	YME1 (S.cerevisiae)-like 1
813410	0.7093173	polymerase (RNA) II (DNA directed) polypeptide K (7.0kD)
826256	0.7092586	transmembrane 7 superfamily member 1 (upregulated in kidney)
124331	0.7081481	cleavage and polyadenylation specific factor 5, 25 kD subunit
770845	0.7068283	hexokinase 1
67765	0.7064266	carboxypeptidase M
207288	0.7058528	insulin induced gene 1
1639531	0.7033264	RAB27A, member RAS oncogene family
731023	0.7032815	WD repeat domain 5
756442	0.7016064	P450 (cytochrome) oxidoreductase
358162	0.6999211	protein predicted by clone 23627
782608	0.698569	mitochondrial ribosomal protein L9
509823	0.6982362	carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen)
345787	0.6981453	highly expressed in cancer, rich in leucine heptad repeats
810402	0.6978141	hypothetical protein

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744417	0.6975761	carnitine acetyltransferase
814306	0.6963874	tumor protein D52
41356	0.6961169	protein phosphatase 2, regulatory subunit B (B56), alpha isoform
813419	0.6951349	hydroxyacyl-Coenzyme A dehydrogenase, type II
629944	0.6950339	myosin VB
327506	0.6943362	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 327506
768064	0.6936336	cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 1
770992	0.693225	
469383	0.6925975	chromosome 8 open reading frame 1
1492780	0.6923749	Homo sapiens cDNA FLJ14459 fis, clone HEMBB1002409
41569	0.691145	hypothetical protein FLJ12650
509588	0.6903363	TATA box binding protein (TBP)-associated factor, RNA polymerase II, J, 20kD
144880	0.6902434	hypothetical protein from EUROIMAGE 1759349
789376	0.6883473	thioredoxin reductase 1
268946	0.6881593	WD40 protein Ciao1
810156	0.6879064	deoxythymidylate kinase (thymidylate kinase)
84295	0.6876167	interleukin 1 receptor antagonist
246800	0.6867481	hypothetical protein FLJ10803
589232	0.6865999	hypothetical protein FLJ11506
859761	0.6846134	poliovirus receptor-related 2 (herpesvirus entry mediator B)
431505	0.6840493	ESTs, Highly similar to A31026 probable membrane receptor protein [H.sapiens]
109863	0.683291	epithelial membrane protein 2
770355	0.6829507	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)
344091	0.6818771	ESTs
813707	0.6814476	regulator of G-protein signalling 16
124781	0.6809199	squalene epoxidase
502774	0.6807524	hypothetical protein FLJ20623
825740	0.6805157	DKFZp434J1813 protein
1536006	0.6805004	ESTs

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203003	0.6802818	non-metastatic cells 4, protein expressed in
785616	0.6800658	signal sequence receptor, alpha (translocon-associated protein alpha)
785840	0.6800437	SEC24 (<i>S. cerevisiae</i>) related gene family, member D
256619	0.6797698	hydroxysteroid (17-beta) dehydrogenase 7
2108077	0.6796871	CGI-112 protein
742595	0.6784804	cyclin-dependent kinase 5
1476065	0.6783519	stathmin 1/oncoprotein 18
68636	0.6778817	hypothetical protein MGC2477
564847	0.6770455	ESTs
744047	0.6748419	polo (<i>Drosophila</i>)-like kinase
897813	0.6741253	polyadenylate binding protein-interacting protein 1
823930	0.6738266	actin related protein 2/3 complex, subunit 1A (41 kD)
236034	0.673506	uncoupling protein 2 (mitochondrial, proton carrier)
743977	0.6729967	Homo sapiens mRNA for TL132
293727	0.6728542	hypothetical protein MGC861
590759	0.672734	sterol-C4-methyl oxidase-like
811024	0.6706275	bone marrow stromal cell antigen 2
785795	0.6683919	hypothetical protein FLJ12910
530310	0.6682042	KIAA0143 protein
1734309	0.666164	sperm associated antigen 4
1898619	0.6651268	hypothetical protein MGC15737
358267	0.6648183	EST, Moderately similar to AF119917 63 PRO2831 [<i>H.sapiens</i>]
753400	0.6633015	CGI-204 protein
292770	0.6609782	Homo sapiens, clone IMAGE:3627860, mRNA, partial cds
884425	0.6608337	chaperonin containing TCP1, subunit 5 (epsilon)
1696757	0.6599512	hypothetical protein KIAA1165
121251	0.6596925	hypothetical protein MGC5576
770785	0.658751	1,2-alpha-mannosidase IC
590774	0.657447	mitogen-activated protein kinase 13
969877	0.6564571	synaptosomal-associated protein, 25kD
415102	0.6562436	cell division cycle 25C
120271	0.6562017	hypothetical protein MGC4692

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713782	0.6552297	a disintegrin and metalloproteinase domain 15 (metargidin)
49351	0.6551453	SEX gene
488642	0.6541915	ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]
343607	0.6510034	AD-015 protein
2306987	0.6501071	secreted and transmembrane 1
280249	0.64759	Kruppel-like factor 7 (ubiquitous)
752631	0.6473517	fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)
489594	0.645574	hypothetical protein FLJ11565
773188	0.6448143	nuclear receptor subfamily 1, group D, member 2
2015517	0.6441737	hypothetical protein FLJ22237
343731	0.6424907	
491524	0.6424448	mitochondrial ribosomal protein L13
824524	0.6424419	UDP-galactose transporter related
593431	0.6422897	ESTs, Moderately similar to CEGT_HUMAN CERAMIDE GLUCOSYLTRANSFERASE [H.sapiens]
812994	0.6420817	retinoid X receptor, alpha
1631735	0.6404771	Homo sapiens, clone IMAGE:3604336, mRNA, partial cds
278531	0.6404612	cytochrome c oxidase subunit VIc
2302099	0.6386686	sialidase 3 (membrane sialidase)
454896	0.6384516	DnaJ (Hsp40) homolog, subfamily A, member 2
1456701	0.6383709	B-cell CLL/lymphoma 9
2055807	0.638184	protein kinase domains containing protein similar to phosphoprotein C8FW
1518402	0.6378481	KIAA1361 protein
810762	0.6371461	SNARE protein
124447	0.6363079	KIAA1184 protein
49273	0.635859	solute carrier family 27 (fatty acid transporter), member 4
365060	0.6350631	RAB11A, member RAS oncogene family
1591264	0.6337293	transaldolase 1
41698	0.6327738	progesterone binding protein
810316	0.6323393	very long-chain acyl-CoA synthetase; lipidosin
826363	0.6322533	lysophospholipase II

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2011515	0.6319712	DKFZP586B0923 protein
770675	0.6315109	Homo sapiens cDNA: FLJ21323 fis, clone COL02374
1461477	0.6300096	Homo sapiens mRNA; cDNA DKFZp586I0324 (from clone DKFZp586I0324)
366834	0.629867	envoplakin
1601947	0.6297475	cytochrome c oxidase subunit VIIa polypeptide 2 (liver)
510575	0.6295917	hypothetical protein FLJ22087
503851	0.6291771	nuclear receptor co-repressor/HDAC3 complex subunit
810063	0.6286184	growth factor, erv1 (S. cerevisiae)-like (augmenter of liver regeneration)
754653	0.6277098	cadherin, EGF LAG seven-pass G-type receptor 3, flamingo (Drosophila) homolog
1518890	0.6251884	metallothionein-like 5, testis-specific (tesmin)
784105	0.6244805	ESTs
205049	0.6231646	protein kinase H11; small stress protein-like protein HSP22
325606	0.6225147	hypothetical protein MGC14353
760299	-1.8441097	dickkopf (Xenopus laevis) homolog 3
200814	-1.8295958	membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)
1882697	-1.715818	peanut (Drosophila)-like 2
344720	-1.6567437	glycophorin C (Gerbich blood group)
1161564	-1.5877154	desmuslin
45099	-1.566311	regucalcin (senescence marker protein-30)
75859	-1.5303427	N-myc downstream-regulated gene 2
811920	-1.5255258	interleukin 11 receptor, alpha
1569187	-1.4872982	heparan sulfate (glucosamine) 3-O-sulfotransferase 4
796542	-1.4697418	ets variant gene 5 (ets-related molecule)
767202	-1.4573536	latent transforming growth factor beta binding protein 2
285377	-1.4496786	pellino (Drosophila) homolog 2
300632	-1.449587	hypothetical protein FLJ21044 similar to Rbig1

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160192	-1.4231519	ESTs, Weakly similar to 2004399A chromosomal protein [H.sapiens]
611532	-1.3689616	troponin I, skeletal, fast
813265	-1.3632094	Homo sapiens mRNA; cDNA DKFZp564H1916 (from clone DKFZp564H1916)
1469377	-1.359583	lipoma HMGIC fusion partner-like 2
810002	-1.3553375	Homo sapiens, clone MGC:19762 IMAGE:3636045, mRNA, complete cds
2056139	-1.3506352	LIM domain protein
377275	-1.3392122	ataxia-telangiectasia group D-associated protein
298122	-1.3364021	frizzled (Drosophila) homolog 7
72778	-1.3299927	caspase 7, apoptosis-related cysteine protease
841308	-1.3246996	myosin, light polypeptide kinase
377461	-1.3214357	caveolin 1, caveolae protein, 22kD
1473274	-1.3200174	myosin regulatory light chain 2, smooth muscle isoform
1554167	-1.3141843	hypothetical protein FLJ14529
131839	-1.3048208	folate receptor 1 (adult)
67741	-1.3014364	PP2135 protein
132857	-1.280579	Homo sapiens mRNA; cDNA DKFZp586N1323 (from clone DKFZp586N1323)
345670	-1.2805684	ESTs, Moderately similar to I59348 CCAAT binding transcription factor CBF subunit C - rat [R.norvegicus]
781014	-1.2659158	suppression of tumorigenicity 5
289760	-1.2610055	ESTs, Highly similar to T00391 hypothetical protein KIAA0612 [H.sapiens]
742685	-1.248683	disabled (Drosophila) homolog 2 (mitogen-responsive phosphoprotein)
52419	-1.2447753	Friedreich ataxia region gene X123
838478	-1.2349342	neurocalcin delta
839736	-1.2337192	crystallin, alpha B
1558675	-1.2313679	SRY (sex determining region Y)-box 10
796181	-1.2276581	growth arrest-specific 6
878836	-1.2200837	secretory granule, neuroendocrine protein 1 (7B2 protein)
130201	-1.2181641	intercellular adhesion molecule 2
1917449	-1.217371	serum amyloid A4, constitutive

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22917	-1.2164705	Homo sapiens mRNA; cDNA DKFZp761M0111 (from clone DKFZp761M0111)
1871116	-1.209237	Homo sapiens mRNA; cDNA DKFZp434C1714 (from clone DKFZp434C1714); partial cds
823871	-1.2090693	SPARC-like 1 (mast9, hevin)
811837	-1.2030392	
811848	-1.2011809	hypothetical protein
840266	-1.200789	Homo sapiens cDNA: FLJ22667 fis, clone HSI08385
753071	-1.2005994	Homo sapiens cDNA: FLJ22528 fis, clone HRC12825
2106144	-1.1719133	regulated in glioma
2504881	-1.1674204	signal transducer and activator of transcription 5A
811837	-1.157587	eukaryotic translation elongation factor 1 alpha 1
486683	-1.1548164	Homo sapiens mRNA; cDNA DKFZp564J0323 (from clone DKFZp564J0323)
712139	-1.1491129	ADP-ribosylation factor-like 7
196435	-1.1475545	ESTs
877621	-1.1422087	nGAP-like protein
811088	-1.140941	ephrin-B3
322561	-1.1270333	ribosomal protein L31
712401	-1.1218827	phosphoinositide-3-kinase, catalytic, delta polypeptide
788234	-1.1061158	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
140574	-1.103064	small inducible cytokine subfamily D (Cys-X3- Cys), member 1 (fractalkine, neurotactin)
490023	-1.1020527	hypothetical protein MGC2648
1584540	-1.0933558	Homo sapiens mRNA; cDNA DKFZp586M2022 (from clone DKFZp586M2022)
1556433	-1.0887923	GRO3 oncogene
47043	-1.0841886	tensin
303109	-1.0807576	purinergic receptor (family A group 5)
343760	-1.0803279	SH3 domain binding glutamic acid-rich protein like 2

[illegible][illegible][illegible]

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270826	-0.9896888	Homo sapiens cDNA FLJ13329 fis, clone OVARC1001795
1257131	-0.9869928	ESTs

Example VII: Genes for discriminating between ADH and DCIS

As shown in Table 6 below, 350 genes were identified as being able to discriminate between ADH and DCIS. The actual data is shown in Figure 3.

Table 6

CloneID	Weight	Description
1404774	-0.5685596	parathyroid hormone-like hormone
823871	-0.9429443	SPARC-like 1 (mast9, hevin)
1882697	-1.4318896	peanut (Drosophila)-like 2
140071	-0.5708303	frizzled-related protein
160192	-1.1751869	ESTs, Weakly similar to 2004399A chromosomal protein [H.sapiens]
796542	-1.2625621	ets variant gene 5 (ets-related molecule)
611532	-1.3158379	troponin I, skeletal, fast
1473274	-1.1172693	myosin regulatory light chain 2, smooth muscle isoform
469306	-0.5113377	gastrin-releasing peptide
2306697	-0.4494025	neuromedin B
132857	-1.0084069	Homo sapiens mRNA; cDNA DKFZp586N1323 (from clone DKFZp586N1323)
2504881	-1.000863	signal transducer and activator of transcription 5A
760299	-1.7010462	dickkopf (Xenopus laevis) homolog 3
293819	-0.4051233	oxidoreductase UCPA
130835	0.3209345	Homo sapiens, Similar to clone FLB3816, clone IMAGE:3454380, mRNA
66532	-0.5773248	endothelin 3
2499829	-0.3619416	zinc finger protein 145 (Kruppel-like, expressed in promyelocytic leukemia)
85840	-0.7754435	nicotinamide N-methyltransferase

sd-71385

10020018 10020018 10020018

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859359	-0.4669761	quinone oxidoreductase homolog
200814	-1.4325283	membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)
825287	-0.2783909	tumor necrosis factor (ligand) superfamily, member 11
202577	-0.2283149	histamine N-methyltransferase
2014373	0.0232775	HNK-1 sulfotransferase
153760	-0.9227865	EphB1
377275	-1.3102234	ataxia-telangiectasia group D-associated protein
745490	-0.6329354	hypothetical protein FLJ20607
172783	-0.6088873	hypothetical protein FLJ10390
1558108	0.0044098	ATP-binding cassette, sub-family C (CFTR/MRP), member 8
1587710	-0.8252065	period (Drosophila) homolog 1
141731	-0.4531468	
490484	-0.3388325	ESTs
504959	-0.1620065	Homo sapiens mRNA; cDNA DKFZp586G0321 (from clone DKFZp586G0321)
1609746	-0.4792809	vitelliform macular dystrophy (Best disease, bestrophin)
882248	-0.8700731	transgelin
1917449	-1.0894686	serum amyloid A4, constitutive
2119838	-0.3045374	a disintegrin-like and metalloprotease (repolysin type) with thrombospondin type 1 motif, 8
841507	0.0247736	surfactant, pulmonary-associated protein A2
813265	-1.2230435	Homo sapiens mRNA; cDNA DKFZp564H1916 (from clone DKFZp564H1916)
767202	-1.0654145	latent transforming growth factor beta binding protein 2
1156538	0.2252628	potassium inwardly-rectifying channel, subfamily J, member 11
39600	-0.6540275	adenylate kinase 5
1630990	-0.7312981	ribosomal protein L29
41208	-0.865227	bone morphogenetic protein 1
322561	-0.7970805	ribosomal protein L31
951008	-0.2221875	ESTs
841308	-0.9953716	myosin, light polypeptide kinase

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119290 -0.8224756 cortic al thymocyte receptor (X. laevis CTX) like
344959 -0.0998837 gene for serine/threonine protein kinase
810331 -0.1389612 quiescin Q6
1161775 -0.7380353 villin 1
625399 -0.9066615 hypothetical protein similar to beta-transducin family
1470657 -0.3557985 deiodinase, iodothyronine, type II
160609 -0.8405669 ESTs
665356 -0.1575968 tumor necrosis factor receptor superfamily, member 11b
(osteoprotegerin)
1584540 -0.9754693 Homo sapiens mRNA; cDNA DKFZp586M2022 (from clone
DKFZp586M2022)
726779 -0.4459955 calponin 1, basic, smooth muscle
296123 -0.2814132 Homo sapiens PRO1851 mRNA, complete cds
190059 -0.634814 guanine nucleotide binding protein (G protein), gamma 7
1471829 -0.7275378 uncharacterized hypothalamus protein HSMNP1
2056139 -1.0673271 LIM domain protein
190753 -0.4423669 ESTs
1968422 -0.5802058 Homo sapiens mRNA full length insert cDNA clone
EUROIMAGE 1968422
725390 -0.4620278 glutathione S-transferase pi
814826 -0.8443265 ESTs
878836 -1.037352 secretory granule, neuroendocrine protein 1 (7B2 protein)
27769 -0.8298821 ESTs
188388 -0.6824191 integrin, alpha 10
1597813 -0.5406089 hypothetical protein PP1044
1609625 -0.5920312 selectin P ligand
810981 -0.1805871 hypothetical protein FLJ20699
726703 -0.070084 Homo sapiens clone 23736 mRNA sequence
781014 -1.0161379 suppression of tumorigenicity 5
898222 0.1795078 Homo sapiens clone 24418 mRNA sequence
1475738 -0.6753091 ribosomal protein S25
1492144 -0.2356446 butyrophilin, subfamily 3, member A2
1492147 -0.636656 ribosomal protein S4, X-linked

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1711456	-0.4896574 H factor (complement)-like 1
1871116	-0.9821709 Homo sapiens mRNA; cDNA DKFZp434C1714 (from clone DKFZp434C1714); partial cds
344720	-1.5196431 glycophorin C (Gerbich blood group)
45099	-1.3515907 regucalcin (senescence marker protein-30)
307029	-0.6500872 ribosomal protein L26
25763	-0.2725443 ankylosis, progressive (mouse) homolog
2502722	-0.3315871 loss of heterozygosity, 11, chromosomal region 2, gene A
1665444	-0.651994 tumor endothelial marker 1 precursor
165837	-0.3443143 translocase of inner mitochondrial membrane 22 (yeast) homolog
502518	-0.4342228 laminin, beta 2 (laminin S)
897963	-0.9775616 phosphatidic acid phosphatase type 2A
120138	0.1570107 J domain containing protein 1
78946	-0.648366 Homo sapiens pyruvate dehydrogenase kinase 4 mRNA, 3' untranslated region, partial sequence
990881	-0.8335353
859192	-0.2265317 vesicle-associated membrane protein 1 (synaptobrevin 1)
712023	-0.5302372 AT-binding transcription factor 1
855586	-0.3944697 nuclear receptor subfamily 3, group C, member 1
52419	-1.0368509 Friedreich ataxia region gene X123
432072	-0.4193898 nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1
1897947	-0.163146 surfactant, pulmonary-associated protein A2
727229	-0.2668972 mitogen-activated protein kinase kinase kinase 4
810358	-0.5403705 acyl-Coenzyme A dehydrogenase, very long chain
154600	-0.0683999 phospholipase C, delta 1
755855	-0.6298333 solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6
323780	-0.8879854 Homo sapiens cDNA FLJ11177 fis, clone PLACE1007402
230560	-0.1803944 ESTs
283173	-0.4293696 EBP50-PDZ interactor of 64 kD

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265853 -0.3519023 Homo sapiens cDNA FLJ11298 fis, clone PLACE1009794

161456 -0.8215502 serum amyloid A1

184022 -0.7070266 amyloid beta (A4) precursor protein-binding, family B,
member 1 (Fe65)

1636523 -0.1496249 glutathione S-transferase subunit 13 homolog

795730 -0.2892776 signal transduction protein (SH3 containing)

1631682 -0.5162406 peptidylprolyl isomerase E (cyclophilin E)

811837 -0.848137

854763 -0.0493902 Homo sapiens cDNA FLJ11341 fis, clone PLACE1010786

50562 -0.0943363 chromosome 8 open reading frame 4

46843 -0.1736687 neuronal Shc adaptor homolog

178137 -0.6839022 ribosomal protein L34

1662279 -0.2290724 plakophilin 1 (ectodermal dysplasia/skin fragility syndrome)

1635062 -0.8243024 DKFZP586A011 protein

293916 -0.3671832 FKBP-associated protein

415613 -0.5528761 DHHC1 protein

80344 -0.8243418 interleukin 7 receptor

1602798 -0.4300808 choline kinase-like

1910516 -0.2845842 ESTs

740620 -0.96496 tropomyosin 2 (beta)

277627 -0.5329107 Human SH3 domain-containing protein SH3P18 mRNA,
complete cds

854696 0.008949 sia binding protein 1; FBP interacting repressor; pyrimidine
tract binding splicing factor; Ro ribonucleoprotein-binding
protein 1

45578 -0.1295485 mitogen-activated protein kinase kinase 6

950710 -0.346361 propionyl Coenzyme A carboxylase, alpha polypeptide

768043 -0.4005598 ECSIT

308539 -0.6726187 Homo sapiens cDNA FLJ12777 fis, clone NT2RP2001720

595637 -0.5373697 Homo sapiens mRNA; cDNA DKFZp586N012 (from clone
DKFZp586N012)

143661 -0.4713778 netrin 4

248631 -0.9106505 aminomethyltransferase (glycine cleavage system protein T)

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826622 0.1339287 KIAA0430 gene product
51981 -0.5554908 ribosomal protein L7a
811848 -1.1350073 hypothetical protein
1533710 -0.5988282 ortholog of mouse integral membrane glycoprotein LIG-1

2017756 -0.2549438 homolog of yeast MOG1
1637296 -0.5105214 ribosomal protein S24
50586 -0.6794282 KIAA1545 protein
877835 -0.5382125 ribosomal protein L35
773319 -0.285447 ribosomal protein S6 kinase, 70kD, polypeptide 1

2014888 -0.2871529 sushi-repeat protein
767495 -0.0366213 GLI-Kruppel family member GLI3 (Greig
cephalopolysyndactyly syndrome)
774078 -0.6508021 leiomodulin 1 (smooth muscle)
868400 -0.4928479 glutamyl-tRNA synthetase
240620 -0.5065007 vascular Rab-GAP/TBC-containing
1588791 -0.1606643 O-6-methylguanine-DNA methyltransferase

472186 -0.2687871 RAB32, member RAS oncogene family
725143 -0.3410957 hypothetical protein FLJ22418
714472 -0.3677387 KIAA0397 gene product
1854648 0.0089186 hemopexin
855029 0.076972 Ac-like transposable element
197727 -0.3906866 phosphatidylethanolamine N-methyltransferase

1623016 -0.6263561 EST
813841 0.0885625 plasminogen activator, tissue
2783721 -0.6854649 cholinergic receptor, nicotinic, beta polypeptide 1 (muscle)

549933 -0.3547881 interleukin 8
280907 -0.7307519 Kruppel-type zinc finger protein
796181 -0.8888496 growth arrest-specific 6
415233 -0.6506593 ribosomal protein L37a
811920 -1.2690713 interleukin 11 receptor, alpha
415415 -0.646492 EST, Moderately similar to RL1X_HUMAN 60S RIBOSOMAL
PROTEIN L18A [H.sapiens]

2018807 -0.2989936 KIAA0468 gene product
154999 -0.3876757 hypothetical protein FLJ21007
68557 0.0637586 fatty acid binding protein 1, liver
647763 -0.1436566 ESTs

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1568967 -0.2938468 ESTs
210717 -0.4522432 syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan)
1350439 -0.6740833 KIAA0015 gene product
684582 -0.0089016 tryptophanyl tRNA synthetase 2 (mitochondrial)
122394 -0.049399 guanine nucleotide binding protein (G protein), alpha 15 (Gq class)
213136 -0.1139004 BTG family, member 2
625458 -0.2394796 hypothetical protein MGC3234
811162 -0.3821116 fibromodulin
1926246 -0.701769 ESTs, Moderately similar to T46371 hypothetical protein DKFZp434P1018.1 [H.sapiens]
1554167 -1.0818834 hypothetical protein FLJ14529
811088 -1.0851546 ephrin-B3
72778 -1.1752838 caspase 7, apoptosis-related cysteine protease
220293 -0.5078291 Homo sapiens cDNA: FLJ21800 fis, clone HEP00618
1569187 -1.2971252 heparan sulfate (glucosamine) 3-O-sulfotransferase 4
866866 -0.4801351 Ras association (RalGDS/AF-6) domain family 1
81316 -0.6176265 ESTs
1161564 -1.3891189 desmuslin
898044 -0.4691863 metallocarboxypeptidase CPX-1
293001 -0.4472585 hypothetical protein DKFZp434E2318
1570502 -0.3314609 Homo sapiens cDNA FLJ12936 fis, clone NT2RP2005018
839796 -0.6807912 candidate tumor suppressor p33 ING1 homolog
380883 -0.4438655 Homo sapiens cDNA FLJ10158 fis, clone HEMBA1003463
180561 -0.3250633 glutathione S-transferase M4
869450 -0.7659922 ribosomal protein L11
47043 -0.7729643 tensin
810463 -0.0829995 DKFZP566O084 protein
149539 0.4138942 KIAA1700
200354 -0.0613983 thymidine kinase 2, mitochondrial
771173 0.1757755 mitochondrial ribosomal protein S21
270826 -0.9389651 Homo sapiens cDNA FLJ13329 fis, clone OVARC1001795

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810017 -0.1076821 plasminogen activator, urokinase receptor
809838 0.0956351
344168 -0.386185 polymerase (DNA directed), lambda
785967 -0.6049171 erythrocyte membrane protein band 4.1-like 2

511831 -0.2912672 hypothetical protein MGC12936
282404 -0.5528532 Homo sapiens mRNA for KIAA1671 protein, partial cds

730036 -0.079736 Mad4 homolog
298231 -0.3550893 gamma-aminobutyric acid (GABA) B receptor, 1

2106144 -1.067765 regulated in glioma
743880 -0.3262292 KIAA0263 gene product
268234 -0.1535073 Dmx-like 1
280776 -0.2922639 acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain

212078 -0.1831462 integrin, alpha 1
731308 0.5371204 citrate synthase
774471 -0.1753902 laminin, beta 1
811837 -0.8764231 eukaryotic translation elongation factor 1 alpha 1

714437 0.0258281 sema domain, immunoglobulin domain (Ig), transmembrane
domain (TM) and short cytoplasmic domain, (semaphorin) 4B

416959 -0.957248 nuclear factor I/B
681992 -0.7691299 Homo sapiens cDNA FLJ13384 fis, clone PLACE1001062,
highly similar to Homo sapiens mRNA for lysine-
ketoglutarate reductase/saccharopine dehydrogenase

130201 -1.0401997 intercellular adhesion molecule 2
363144 0.1937891 transcription factor AP-2 beta (activating enhancer-binding
protein 2 beta)
857874 -0.3703645 transforming growth factor beta-activated kinase-binding
protein 1
377461 -1.2798035 caveolin 1, caveolae protein, 22kD
156363 0.2685238 hypothetical protein FLJ12934
589115 -0.0115547 matrix metalloproteinase 1 (interstitial collagenase)

241489 -0.6212938 adrenergic, beta-2-, receptor, surface
586725 0.0683397 protein phosphatase 2, regulatory subunit B (B56), beta
isoform

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283124	-0.7933772 ESTs, Moderately similar to LONG-CHAIN FATTY ACID TRANSPORT PROTEIN [M.musculus]
307328	-0.4022704 hypothetical protein FLJ10948
37449	-0.3539978 GAS2-related on chromosome 22
50892	-0.6887497 Homo sapiens, clone MGC:9913 IMAGE:3870821, mRNA, complete cds
1897944	-0.4855156 ESTs, Weakly similar to T00366 hypothetical protein KIAA0669 [H.sapiens]
377314	-0.561312 casein kinase 2, alpha prime polypeptide
220851	-0.0351418 crystallin, alpha A
322233	-0.3025167
586803	-0.7423407 placental growth factor, vascular endothelial growth factor- related protein
343695	-0.7706809 hypothetical protein FLJ10875
414999	-0.5002542 ets variant gene 4 (E1A enhancer-binding protein, E1AF)
813823	-0.4463267 lumican
178825	-0.1525189 neurogranin (protein kinase C substrate, RC3)
85582	-0.0716296 target of myb1 (chicken) homolog-like 2
753620	-0.5248489 insulin-like growth factor binding protein 6
1899338	-0.066168 mannosidase, alpha, class 1A, member 2
359250	0.0674486 carbonic anhydrase IV
345034	-1.0600859 small inducible cytokine subfamily B (Cys-X-Cys), member 14 (BRAK)
2164744	-0.2307289 neural cell adhesion molecule 1
613056	-0.3957342 reticulocalbin 1, EF-hand calcium binding domain
1410444	-0.0368027 amphiregulin (schwannoma-derived growth factor)
593023	-0.7516846 dystrobrevin, beta
788511	0.1403148 ribosomal protein S6 kinase, 90kD, polypeptide 1
455269	0.0223607
1650927	-0.1712163 hypothetical protein DKFZp547E052
782427	-0.2818886 inhibin, beta B (activin AB beta polypeptide)
71727	-0.2796517 T-cell acute lymphocytic leukemia 1
840942	-0.6383764 major histocompatibility complex, class II, DP beta 1
825470	0.5218731 topoisomerase (DNA) II alpha (170kD)

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595213	0.4824381 hypothetical protein
796694	0.6893307 baculoviral IAP repeat-containing 5 (survivin)
810711	0.9128832 stearoyl-CoA desaturase (delta-9-desaturase)
629944	0.5273447 myosin VB
66406	0.5966701 hypothetical protein DKFZp762E1312
785840	0.5401209 SEC24 (S. cerevisiae) related gene family, member D
210862	0.4683996 acyl-Coenzyme A oxidase 1, palmitoyl
84295	0.3989864 interleukin 1 receptor antagonist
429182	0.2952867 dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit
705064	0.4497555 transforming, acidic coiled-coil containing protein 3
782513	0.4759571 interferon, alpha-inducible protein (clone IFI-6-16)
839682	0.5208954 ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13)
768377	0.3809674 activity-dependent neuroprotective protein
2309073	0.5226599 frizzled (Drosophila) homolog 5
789376	0.4339171 thioredoxin reductase 1
196992	-0.1015205 aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)
785707	0.4708376 protein regulator of cytokinesis 1
1505038	1.1904802 hypothetical protein FLJ20171
869375	0.4827093 isocitrate dehydrogenase 2 (NADP+), mitochondrial
109221	0.3048287 KIAA0286 protein
345787	0.4647372 highly expressed in cancer, rich in leucine heptad repeats
46248	0.640944 ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase)
79520	0.6769129 RAB2, member RAS oncogene family
469383	0.5558732 chromosome 8 open reading frame 1
509588	0.4157059 TATA box binding protein (TBP)-associated factor, RNA polymerase II, J, 20kD
292936	0.4217115 hypothetical protein FLJ10468
686172	0.6724684 KIAA0008 gene product
788655	0.2976191 HTPAP protein

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770992	0.3331315
1587847	0.1732392 minichromosome maintenance deficient (mis5, S. pombe) 6
79710	0.4579008 KIAA0174 gene product
2056566	0.2341905 integrin, alpha M (complement component receptor 3, alpha; also known as CD11b (p170), macrophage antigen alpha polypeptide)
454339	0.3738929 thiopurine S-methyltransferase
594226	0.403676 Homo sapiens cDNA FLJ14459 fis, clone HEMBB1002409
897813	0.4749348 polyadenylate binding protein-interacting protein 1
824694	0.0268936 protein tyrosine phosphatase type IVA, member 1
725454	0.6669973 CDC28 protein kinase 2
79254	0.0732432 MHC class I region ORF
1472719	0.2550065 SMT3 (suppressor of mif two 3, yeast) homolog 1
2054635	0.7914755 proteasome (prosome, macropain) subunit, alpha type, 7
289978	0.6308861 ubiquitin-like 4
155806	0.2747101 2'-5'-oligoadenylate synthetase 2 (69-71 kD)
147834	0.4412795 zinc finger protein 217
26171	0.3656147 KIAA0856 protein
2322367	0.5832711 reticulon 4
769921	0.6464245 ubiquitin carrier protein E2-C
73009	0.4822587 ESTs, Weakly similar to A43932 mucin 2 precursor, intestinal [H.sapiens]
2014034	0.6620303 methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase
359887	0.8692353 translocase of inner mitochondrial membrane 17 (yeast) homolog A
488964	0.9569176 H2A histone family, member O
1476065	0.289904 stathmin 1/oncoprotein 18
1422338	0.5874097 ribonucleotide reductase M2 polypeptide
268946	0.5440003 WD40 protein Ciao1
686552	0.7231319 golgi phosphoprotein 1
149544	0.283642 neuroepithelial cell transforming gene 1
770675	0.454729 Homo sapiens cDNA: FLJ21323 fis, clone COL02374

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346257 0.1515899 minichromosome maintenance deficient (*S. cerevisiae*) 4
429799 0.6915155 hypothetical protein FLJ21939 similar to 5-azacytidine
induced gene 2
143997 0.1883447 proteasome (prosome, macropain) 26S subunit, non-
ATPase, 10
122241 0.7394284 proteasome (prosome, macropain) subunit, beta type, 2
823598 0.9153521 proteasome (prosome, macropain) 26S subunit, non-
ATPase, 12
814632 0.0960611 splicing factor, arginine/serine-rich (transformer 2 *Drosophila*
homolog) 10
810316 0.3732635 very long-chain acyl-CoA synthetase; lipidosin
290841 0.8346933 H2B histone family, member A
347373 0.7563599 transcription elongation factor B (SIII), polypeptide 1 (15kD,
elongin C)
700792 0.4949149 cyclin-dependent kinase inhibitor 3 (CDK2-associated dual
specificity phosphatase)
1554549 0.9764206 hydroxyacyl glutathione hydrolase
897770 0.4270685
504308 0.5564295 hypothetical protein FLJ10540
132828 0.2875519 Down syndrome critical region gene 1-like 2
292388 0.112577
1616253 0.567837 breast carcinoma amplified sequence 1
796469 1.0269115 HSPC150 protein similar to ubiquitin-conjugating enzyme
2139152 -0.4373776 Homo sapiens clone 24473 mRNA sequence
130276 0.2154295 Homo sapiens mRNA; cDNA DKFZp586H0324 (from clone
DKFZp586H0324)
34149 0.309569 KIAA0227 protein
150003 0.8251408 hypothetical protein FLJ13187
287749 0.3173706 CDC7 (cell division cycle 7, *S. cerevisiae*, homolog)-like 1
25380 0.164077 ESTs, Moderately similar to JC5238 galactosylceramide-like
protein, GCP [*H.sapiens*]
745083 0.4107735 ubiquitin specific protease 18
810899 0.240336 CDC28 protein kinase 1
768059 0.3139886 hypothetical protein FLJ12619

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815026	0.4472842	cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kD
741474	0.7732047	glucose phosphate isomerase
788641	0.3638059	adaptor-related protein complex 1, sigma 2 subunit
2043167	0.7167431	BCL2-associated athanogene 3
1492780	0.6544659	Homo sapiens cDNA FLJ14459 fis, clone HEMBB1002409
2306987	0.4402912	secreted and transmembrane 1
754653	0.4405873	cadherin, EGF LAG seven-pass G-type receptor 3, flamingo (Drosophila) homolog
743810	0.3667087	hypothetical protein MGC2577
126858	0.2389814	sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1
2017415	0.43546	centromere protein A (17kD)
280507	0.2846518	hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)
67237	0.1406869	ESTs
43833	-0.1197546	diacylglycerol kinase, gamma (90kD)
42076	0.3194462	TRK-fused gene
531319	0.1093932	serine/threonine kinase 12
784129	0.2902598	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide
586895	0.2549108	small nuclear ribonucleoprotein polypeptide G

Example VIII: Genes for discriminating between DCIS Grade I and Grade III

As shown in Table 7 below, 350 genes were identified as being able to discriminate between grades of DCIS. The actual data corresponding to this table is shown in Figure 4.

Table 7

CloneID	Weight	Description
2460159	4.6268975	tyrosine kinase, non-receptor, 1
358151	2.8783989	zinc finger protein 33a (KOX 31)

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795382 2.772572 Rap1 guanine-nucleotide-exchange factor directly activated by
cAMP
714472 2.6829714 KIAA0397 gene product
725649 2.6433625 nuclear factor of activated T-cells, cytoplasmic, calcineurin-
dependent 4
51218 2.6200167 ESTs
504959 2.5777963 Homo sapiens mRNA; cDNA DKFZp586G0321 (from clone
DKFZp586G0321)

647397 2.5320153 ESTs
814815 2.4198892 plakophilin 4
279720 2.4136316 ESTs, Moderately similar to A47582 B-cell growth factor
precursor [H.sapiens]
298231 2.4096172 gamma-aminobutyric acid (GABA) B receptor, 1

172783 2.3339699 hypothetical protein FLJ10390
261609 2.311051 ESTs, Weakly similar to S65657 alpha-1C-adrenergic receptor
splice form 2 [H.sapiens]

826668 2.2951137 KIAA0274 gene product
1493383 2.2616737 Homo sapiens mRNA; cDNA DKFZp434H2418 (from clone
DKFZp434H2418)

2017756 2.2403622 homolog of yeast MOG1
1455566 2.1756946 adenosine A3 receptor
725321 2.1658095 estrogen receptor 1
180561 2.1393944 glutathione S-transferase M4
32050 2.1165022 Homo sapiens mRNA; cDNA DKFZp586P1124 (from clone
DKFZp586P1124)

215000 2.1150123 vasoactive intestinal peptide receptor 1
2019750 2.0957741 SEC14 (S. cerevisiae)-like 2
283124 2.0921779 ESTs, Moderately similar to LONG-CHAIN FATTY ACID
TRANSPORT PROTEIN [M.musculus]

490615 2.0635424 tubulin, gamma 2
666138 2.0625667 hypothetical protein DKFZp761J1523
418129 2.0541212 nuclear mitotic apparatus protein 1
1733262 2.052666 BLu protein
1588791 2.044069 O-6-methylguanine-DNA methyltransferase

461761 2.035953 angiogenin, ribonuclease, RNase A family, 5

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1031592 1.9930012 kinesin protein 9 gene
126415 1.9781057 Homo sapiens mRNA; cDNA DKFZp566H0124 (from clone
DKFZp566H0124)

28643 1.9733043 hypothetical protein DKFZp564D1378
470261 1.9160486
1630990 1.9155421 ribosomal protein L29
810981 1.9132205 hypothetical protein FLJ20699
767495 1.9052671 GLI-Kruppel family member GLI3 (Greig
cephalopolysyndactyly syndrome)
767176 1.8996792 tumor necrosis factor (ligand) superfamily, member 13

1572196 1.8855996 secreted modular calcium-binding protein 2

1706635 1.8754346 bone gamma-carboxyglutamate (gla) protein (osteocalcin)

186301 1.8424458 Homo sapiens cDNA FLJ12924 fis, clone NT2RP2004709

726703 1.842399 Homo sapiens clone 23736 mRNA sequence

214205 1.8416657 Homo sapiens, clone MGC:17687 IMAGE:3865868, mRNA,
complete cds
784178 1.822159 Homo sapiens mRNA; cDNA DKFZp586M0723 (from clone
DKFZp586M0723)

346902 1.8196723 ESTs, Weakly similar to ALU2_HUMAN ALU SUBFAMILY SB
SEQUENCE CONTAMINATION WARNING ENTRY
[H.sapiens]

1367678 1.8184255 KIAA0356 gene product
190059 1.7988757 guanine nucleotide binding protein (G protein), gamma 7

1456937 1.7980645 oviductal glycoprotein 1, 120kD (mucin 9, oviductin)

45578 1.7935215 mitogen-activated protein kinase kinase 6
248631 1.7701919 aminomethyltransferase (glycine cleavage system protein T)

1562231 1.7668811 SET binding protein 1
154466 1.7516237 STIP1 homology and U-Box containing protein 1

2524445 1.7392197 neuronal PAS domain protein 1
277266 1.7307752 Homo sapiens, clone IMAGE:3625550, mRNA, partial cds

741891 1.7297992 RAB2, member RAS oncogene family-like

sd-71385

"485772004" Bt02001

206217	1.7227658 nuclear receptor subfamily 1, group H, member 3
2028876	1.7128178 splicing factor, arginine/serine-rich 5
730036	1.70573 Mad4 homolog
1558233	1.7035129 ESTs
502518	1.7027287 laminin, beta 2 (laminin S)
356835	1.7014349 hypothetical protein MGC10500
744994	1.6938348 hypothetical protein FLJ12242
810358	1.6924263 acyl-Coenzyme A dehydrogenase, very long chain
813854	1.6914133 purine-rich element binding protein A
768043	1.6854123 ECSIT
264632	1.6591646 ESTs
505243	1.6581518 inositol 1,4,5-triphosphate receptor, type 2
344073	1.6571604 ESTs, Weakly similar to K1CI_HUMAN KERATIN, TYPE I CYTOSKELETAL 9 [H.sapiens]
343760	1.6435915 SH3 domain binding glutamic acid-rich protein like 2
1569418	1.6408767 Homo sapiens cDNA FLJ11385 fis, clone HEMBA1000520
202577	1.6393518 histamine N-methyltransferase
823634	1.6366047 ESTs
839796	1.630887 candidate tumor suppressor p33 ING1 homolog
183440	1.6297915 arylsulfatase A
344959	1.6268043 gene for serine/threonine protein kinase
1574252	1.6211224 DKFZP586D0623 protein
669359	1.6174855 Homo sapiens clone 24405 mRNA sequence
74070	1.6096611 endosulfine alpha
1660649	1.6051582 suppressor of white apricot homolog 2
796723	1.6041219 Homo sapiens clone CDABP0014 mRNA sequence
743146	1.597094 hypothetical protein FLJ23403
789147	1.5937127 enolase 2, (gamma, neuronal)
342181	1.5926355 B-cell CLL/lymphoma 2
33076	1.5824352 cholinephosphotransferase 1
782497	1.5804781 Homo sapiens, clone IMAGE:3010666, mRNA, partial cds
470261	1.5751564 SMA5
809507	1.5723669 hypothetical protein FLJ20568
712460	1.5721924 natural killer-tumor recognition sequence

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293569 1.5662317 chromosome 1 open reading frame 21
1518402 1.5627158 KIAA1361 protein
155072 1.5557559 ESTs
455269 1.5538593
262804 1.5532348 hypothetical protein MGC2941
1492238 1.5484044 HSPC003 protein
364865 1.5483958 hypothetical protein FLJ21062
2325804 1.5461823 95 kDa retinoblastoma protein binding protein

1635062 1.5449944 DKFZP586A011 protein
344168 1.5421405 polymerase (DNA directed), lambda
1517171 1.5381921 interleukin 2 receptor, alpha
769600 1.5335878 uracil-DNA glycosylase 2
325583 1.5245817 EST
814826 1.5223296 ESTs
1570502 1.5184543 Homo sapiens cDNA FLJ12936 fis, clone NT2RP2005018

511831 1.5183298 hypothetical protein MGC12936
124922 1.5052004 KRAB-zinc finger protein SZF1-1
2072768 1.4886791 nuclear receptor coactivator 3
2021882 1.4854251 sodium channel, nonvoltage-gated 1, delta
627248 1.4827018 SBBI31 protein
725503 1.476461 D-dopachrome tautomerase
285312 1.4699425
141731 1.469088
1456701 1.4668054 B-cell CLL/lymphoma 9
898222 1.4667947 Homo sapiens clone 24418 mRNA sequence

725284 1.4638006 phosphorylase kinase, gamma 2 (testis)
154999 1.4564204 hypothetical protein FLJ21007
1592530 1.4558873 mammalian inositol hexakisphosphate kinase 2

590310 1.4534138 Homo sapiens mRNA; cDNA DKFZp434E2321 (from clone
DKFZp434E2321); partial cds

416042 1.446691 ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J
SEQUENCE CONTAMINATION WARNING ENTRY
[H.sapiens]

2017144 1.4450059 CGI-41 protein
309449 1.4412699 ribosomal protein S4, Y-linked
450301 1.4403678 mutL (E. coli) homolog 3

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1492468 1.4375076 DEME-6 protein
121454 1.4361788 arachidonate 12-lipoxygenase
743880 1.4294838 KIAA0263 gene product
1568967 1.4109448 ESTs
1568989 1.4094472 ESTs
25274 1.4078252 g20 protein
2413337 1.4058288 sortilin-related receptor, L(DLR class) A repeats-containing

197913 1.3994468 splicing factor proline/glutamine rich (polypyrimidine tract-binding protein-associated)

292770 1.3952057 Homo sapiens, clone IMAGE:3627860, mRNA, partial cds

143332 1.3875805 neuropeptide Y receptor Y1
809779 1.3848708 KIAA0239 protein
138242 1.3820433 ESTs, Moderately similar to MAS2_HUMAN MANNAN-BINDING LECTIN SERINE PROTEASE 2 PRECURSOR [H.sapiens]

270127 1.3786197
49240 1.3772023 KIAA0460 protein
826622 1.3734143 KIAA0430 gene product
1858837 1.3719341 ESTs
1583198 1.3712112 ESTs, Weakly similar to S65824 reverse transcriptase homolog [H.sapiens]

345858 1.3629187 cisplatin resistance associated
208387 1.3597205 KIAA1407 protein
502782 1.3589088 RAN binding protein 3
26294 1.3578289 RNB6
669379 1.3559931 Homo sapiens BAC clone RP11-505D17 from 7p22-p21

810728 1.355262 hypothetical gene ZD52F10
1601845 1.3533864 Ca²⁺-promoted Ras inactivator
840882 1.350538 nucleotide binding protein
82173 1.3485351 MYLE protein
490965 1.3476943 ESTs
811162 1.3450626 fibromodulin
61061 1.3437368 hypothetical protein FLJ20585
49630 1.3412751 calcium channel, voltage-dependent, L type, alpha 1D subunit

825659 -2.8345933 N-myc downstream regulated
769921 -2.712812 ubiquitin carrier protein E2-C

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788232 -2.6550962 sestrin 2
1476053 -2.529039 RAD51 (S. cerevisiae) homolog (E coli RecA homolog)
809557 -2.4910488 minichromosome maintenance deficient (S. cerevisiae) 3
150897 -2.4302462 UDP-GlcNAc:betaGal beta-1,3-N-
acetylglucosaminyltransferase 3
814526 -2.37273 seb4D
796694 -2.3104815 baculoviral IAP repeat-containing 5 (survivin)
814792 -2.3001334 ubiquitin specific protease 10
1536236 -2.2971152 hypothetical protein FLJ13154
2017415 -2.2748559 centromere protein A (17kD)
210862 -2.2408114 acyl-Coenzyme A oxidase 1, palmitoyl
795543 -2.2403389 thioredoxin peroxidase (antioxidant enzyme)
773301 -2.2239527 cadherin 3, type 1, P-cadherin (placental)
700792 -2.2203557 cyclin-dependent kinase inhibitor 3 (CDK2-associated dual
specificity phosphatase)
1883327 -2.2093248 ESTs
1523225 -2.1936598 oncostatin M receptor
208718 -2.1882654 annexin A1
1702742 -2.1567809 solute carrier family 7 (cationic amino acid transporter, y+
system), member 5
753378 -2.151145 hypothetical protein FLJ22649 similar to signal peptidase
SPC22/23
429222 -2.1351022 CGI-107 protein
292388 -2.1343367
781047 -2.1262682 budding uninhibited by benzimidazoles 1 (yeast homolog)
450854 -2.0819596 craniofacial development protein 1
823598 -2.0693353 proteasome (prosome, macropain) 26S subunit, non-ATPase,
12
1422338 -2.0689327 ribonucleotide reductase M2 polypeptide
705064 -2.0601901 transforming, acidic coiled-coil containing protein 3
770675 -2.0272207 Homo sapiens cDNA: FLJ21323 fis, clone COL02374
345787 -1.9992897 highly expressed in cancer, rich in leucine heptad repeats
471196 -1.9985751 integral membrane protein 3

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128711 -1.7791673 anillin (Drosophila Scraps homolog), actin binding protein
308633 -1.7667341 hypothetical protein FLJ10339
884425 -1.761486 chaperonin containing TCP1, subunit 5 (epsilon)
745394 -1.7583344 Homo sapiens cDNA: FLJ23249 fis, clone COL04196
852829 -1.7579704 karyopherin alpha 3 (importin alpha 4)
122241 -1.7490794 proteasome (prosome, macropain) subunit, beta type, 2
307255 -1.7294781 basement membrane-induced gene
32493 -1.7273675 integrin, alpha 6
454896 -1.7216328 DnaJ (Hsp40) homolog, subfamily A, member 2
1876217 -1.7186822 DnaJ (Hsp40) homolog, subfamily A, member 2
815556 -1.7161709 hypothetical protein FLJ10430
589869 -1.7120206 transcriptional co-activator with PDZ-binding motif (TAZ)
2012523 -1.7104314 fatty acid binding protein 5 (psoriasis-associated)
1946448 -1.7092537 caveolin 2
841370 -1.7047297 glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate
aminotransferase 2)
1600239 -1.6989076 HSPC037 protein
462926 -1.6981004 NIMA (never in mitosis gene a)-related kinase 2
144880 -1.6980733 hypothetical protein from EUROIMAGE 1759349
744047 -1.6910803 polo (Drosophila)-like kinase
624627 -1.6888444 ribonucleotide reductase M2 polypeptide
788566 -1.6752673 Purkinje cell protein 4
858293 -1.6732706 tyrosine 3-monooxygenase/tryptophan 5-monooxygenase
activation protein, theta polypeptide
470148 -1.659943 ESTs
66902 -1.6546363 ESTs
77533 -1.6505418 inositol polyphosphate-5-phosphatase, 40kD
825282 -1.6417354 DKFZP586L0724 protein
785840 -1.6406565 SEC24 (S. cerevisiae) related gene family, member D

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824962 -1.6399941 karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
741139 -1.6396499 eyes absent (Drosophila) homolog 2
809530 -1.6264151 minichromosome maintenance deficient (S. cerevisiae) 2
(mitotin)
2054635 -1.6254343 proteasome (prosome, macropain) subunit, alpha type, 7
813533 -1.6215197 syndecan binding protein (syntenin)
267816 -1.6173276 KIAA0551 protein
306318 -1.6083862 origin recognition complex, subunit 6 (yeast homolog)-like
796469 -1.6065509 HSPC150 protein similar to ubiquitin-conjugating enzyme
813256 -1.6027042 ATP-binding cassette, sub-family B (MDR/TAP), member 1
843121 -1.60128 chloride intracellular channel 1
713685 -1.6006729 protease, serine, 2 (trypsin 2)
811590 -1.6001102 hypothetical protein FLJ11100
823756 -1.5995448 mitogen inducible 2
549073 -1.597146 capping protein (actin filament) muscle Z-line, alpha 2
743810 -1.5960999 hypothetical protein MGC2577
377368 -1.5955102 cell death regulator aven
1506046 -1.5918448 hypothetical protein FLJ10815
814270 -1.5890389 polymyositis/scleroderma autoantigen 1 (75kD)
1604703 -1.5853167 major histocompatibility complex, class I, F
234736 -1.5765159 GATA-binding protein 6
429182 -1.5699689 dolichyl-phosphate mannosyltransferase polypeptide 1,
catalytic subunit
826355 -1.5677013 vesicle-associated membrane protein 5 (myobrevin)
34149 -1.5659923 KIAA0227 protein
746190 -1.5635857 hypothetical protein DKFZp761B1514
131091 -1.558448 Not56 (D. melanogaster)-like protein
665384 -1.5550415 KIAA1609 protein
625683 -1.5501423 neighbor of COX4
1582738 -1.544427 uncharacterized bone marrow protein BM040
949988 -1.5437326 Homo sapiens mRNA; cDNA DKFZp586E1124 (from clone
DKFZp586E1124); complete cds

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133213 -1.5433392 fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)
1660666 -1.5423907 carbonic anhydrase VB, mitochondrial
713158 -1.5372729 ESTs
1614140 -1.5341302 Ris
201890 -1.5333626 baculoviral IAP repeat-containing 3
38925 -1.5304604 ESTs, Moderately similar to A47582 B-cell growth factor precursor [H.sapiens]
511850 -1.5294752 proteasome (prosome, macropain) 26S subunit, ATPase, 1
489489 -1.5169076 lamin B receptor
825470 -1.5154306 topoisomerase (DNA) II alpha (170kD)
42831 -1.5136459 N-terminal kinase-like
809784 -1.5066053 kallikrein 6 (neurosin, zyme)
730410 -1.506168 lymphocyte-specific protein tyrosine kinase
810983 -1.5060386 DKFZP434H132 protein
731223 -1.5058799 proteasome (prosome, macropain) subunit, beta type, 2
259017 -1.5053827 ESTs
340745 -1.5041978 ESTs
746163 -1.5000358 ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J
SEQUENCE CONTAMINATION WARNING ENTRY
[H.sapiens]
1466621 -1.4998321 ATPase, Ca++ transporting, type 2C, member 1
809588 -1.49754 gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase)
813707 -1.4946872 regulator of G-protein signalling 16
188335 -1.4895328 egf-like module containing, mucin-like, hormone receptor-like sequence 2
1493160 -1.4851884 small inducible cytokine subfamily B (Cys-X-Cys), member 10
531886 -1.4842053 Homo sapiens clone FLB3344 PRO0845 mRNA, complete cds
753428 -1.4835152 Homo sapiens, clone IMAGE:3542597, mRNA, partial cds
897731 -1.4833877 latrophilin
376551 -1.4811859 ETAA16 protein
256907 -1.4755682 glutathione S-transferase A3
712139 -1.4735772 ADP-ribosylation factor-like 7

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785368 -1.4680554 PDZ-binding kinase; T-cell originated protein kinase
825606 -1.4667088 kinesin-like 1
531319 -1.4659871 serine/threonine kinase 12
66406 -1.4641179 hypothetical protein DKFZp762E1312
470124 -1.4635711 RAD1 (S. pombe) homolog

Example IX: Genes for discriminating between IDC Grade I and Grade III

As shown in Table 8 below, 300 genes were identified as being able to discriminate between two grades of IDC.

Table 8

CloneID	Weight	Description
1706635	3.279305	bone gamma-carboxyglutamate (gla) protein (osteocalcin)
666138	3.1366533	hypothetical protein DKFZp761J1523
795382	3.0005724	Rap1 guanine-nucleotide-exchange factor directly activated by cAMP
364865	2.8512705	hypothetical protein FLJ21062
1500542	2.8021264	regulator of G-protein signalling 11
270127	2.7455118	
588262	2.7127609	Homo sapiens, Similar to RIKEN cDNA 2600001A11 gene, clone MGC:9907 IMAGE:3870073, mRNA, complete cds
277266	2.5004627	Homo sapiens, clone IMAGE:3625550, mRNA, partial cds
2090129	2.4882736	chromobox homolog 2 (Drosophila Pc class)
325583	2.4558352	EST
358151	2.4309122	zinc finger protein 33a (KOX 31)
786675	2.3877233	epididymis-specific, whey-acidic protein type, four-disulfide core; putative ovarian carcinoma marker
854763	2.378956	Homo sapiens cDNA FLJ11341 fis, clone PLACE1010786
1592976	2.3417116	microphthalmia-associated transcription factor

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1562231 2.286418 SET binding protein 1
767176 2.2472282 tumor necrosis factor (ligand) superfamily, member 13

784178 2.2026739 Homo sapiens mRNA; cDNA DKFZp586M0723 (from clone
DKFZp586M0723)

811162 2.1926501 fibromodulin
502518 2.1886432 laminin, beta 2 (laminin S)
754429 2.1363368 ESTs, Weakly similar to T00084 hypothetical protein
KIAA0512 [H.sapiens]
214205 2.1127961 Homo sapiens, clone MGC:17687 IMAGE:3865868, mRNA,
complete cds
61061 2.1046094 hypothetical protein FLJ20585
344959 2.0756965 gene for serine/threonine protein kinase
814815 2.0694714 plakophilin 4
262804 2.0673444 hypothetical protein MGC2941
1455566 2.0489061 adenosine A3 receptor
1469149 1.9778151 Homo sapiens clone 24606 mRNA sequence

358217 1.9703763 glypican 4
206217 1.9595484 nuclear receptor subfamily 1, group H, member 3

261609 1.958083 ESTs, Weakly similar to S65657 alpha-1C-adrenergic receptor
splice form 2 [H.sapiens]

197525 1.9550731 flavin containing monooxygenase 5
857640 1.9532398 collagen, type VI, alpha 2
812143 1.9469226 fibronectin leucine rich transmembrane protein 3

898222 1.9409805 Homo sapiens clone 24418 mRNA sequence

418129 1.9385868 nuclear mitotic apparatus protein 1
2021882 1.9213983 sodium channel, nonvoltage-gated 1, delta
293819 1.919948 oxidoreductase UCPA
203003 1.8989675 non-metastatic cells 4, protein expressed in

705274 1.8986548 diacylglycerol kinase, delta (130kD)
124922 1.8975916 KRAB-zinc finger protein SZF1-1
2505310 1.8859615 calcium/calmodulin-dependent protein kinase I

1492238 1.8795818 HSPC003 protein
810358 1.8732889 acyl-Coenzyme A dehydrogenase, very long chain

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2391494 1.8698169 ephrin-A4
1592530 1.8669954 mammalian inositol hexakisphosphate kinase 2

810671 1.8659671 hypothetical protein FLJ22269
2108048 1.8648249 DNB5
730036 1.8564918 Mad4 homolog
810741 1.831265 GABA(A) receptor-associated protein
45578 1.8274273 mitogen-activated protein kinase kinase 6
647397 1.8263711 ESTs
767495 1.8149096 GLI-Kruppel family member GLI3 (Greig
cephalopolysyndactyly syndrome)
32050 1.8117146 Homo sapiens mRNA; cDNA DKFZp586P1124 (from clone
DKFZp586P1124)

811848 1.8106436 hypothetical protein
186301 1.8021505 Homo sapiens cDNA FLJ12924 fis, clone NT2RP2004709

366526 1.7836259 ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAMILY SC
SEQUENCE CONTAMINATION WARNING ENTRY
[H.sapiens]

813154 1.7815662 nuclear factor I/A
85195 1.778695 growth arrest and DNA-damage-inducible, gamma

2460159 1.7730834 tyrosine kinase, non-receptor, 1
504959 1.7723846 Homo sapiens mRNA; cDNA DKFZp586G0321 (from clone
DKFZp586G0321)

742094 1.7684813 hypothetical protein FLJ20950
256619 1.7658619 hydroxysteroid (17-beta) dehydrogenase 7
726699 1.7594888 ESTs, Weakly similar to AAB47496 NG5 [H.sapiens]

2017144 1.7514699 CGI-41 protein
74070 1.7336683 endosulfine alpha
1762111 1.7236006 natriuretic peptide receptor C/guanylate cyclase C
(atrionatriuretic peptide receptor C)

795750 1.7116475 Homo sapiens clone 25056 mRNA sequence

2019750 1.7095011 SEC14 (S. cerevisiae)-like 2
2325804 1.7039903 95 kDa retinoblastoma protein binding protein

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279720 1.693594 ESTs, Moderately similar to A47582 B-cell growth factor precursor [H.sapiens]
132857 1.6875688 Homo sapiens mRNA; cDNA DKFZp586N1323 (from clone DKFZp586N1323)
1898619 1.684954 hypothetical protein MGC15737
681992 1.6802347 Homo sapiens cDNA FLJ13384 fis, clone PLACE1001062, highly similar to Homo sapiens mRNA for lysine-ketoglutarate reductase/saccharopine dehydrogenase
85450 1.6753438 acyl-Coenzyme A oxidase 2, branched chain
51218 1.6748931 ESTs
1925280 1.6563658 homologous to yeast nitrogen permease (candidate tumor suppressor)
250883 1.6504115 ubiquitin-activating enzyme E1-like
172783 1.6502064 hypothetical protein FLJ10390
208387 1.6498608 KIAA1407 protein
703964 1.6452497 inositol polyphosphate phosphatase-like 1
298231 1.6428171 gamma-aminobutyric acid (GABA) B receptor, 1
277848 1.6407233 ADP-ribosylation factor 6
669359 1.6386236 Homo sapiens clone 24405 mRNA sequence
321455 1.6327309 Homo sapiens, Similar to RIKEN cDNA 1110002C08 gene, clone MGC:9564 IMAGE:3872267, mRNA, complete cds
796152 1.6295159 Homo sapiens cDNA FLJ11685 fis, clone HEMBA1004934
502782 1.614818 RAN binding protein 3
360778 1.6091782
950574 1.606032 H3 histone, family 3B (H3.3B)
788334 1.5816572 mitochondrial ribosomal protein L23
782497 1.5767626 Homo sapiens, clone IMAGE:3010666, mRNA, partial cds
1733262 1.5656438 BLu protein
342181 1.5642436 B-cell CLL/lymphoma 2
1632248 1.5590794 Homo sapiens cDNA FLJ14181 fis, clone NT2RP2004300
1526826 1.5576997 homeo box B2
145132 1.5520317 mannose-P-dolichol utilization defect 1
183062 1.5400324 ubiquitin specific protease 21

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823663	1.5337257 fragile X mental retardation, autosomal homolog 2
190059	1.5258594 guanine nucleotide binding protein (G protein), gamma 7
111721	1.5045285 insulin induced protein 2
840882	1.5039692 nucleotide binding protein
1902764	1.5037016 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3
414999	1.5021506 ets variant gene 4 (E1A enhancer-binding protein, E1AF)
1636523	1.4948923 glutathione S-transferase subunit 13 homolog
594683	1.4862053 ESTs
1916575	1.4825298 BCL2-interacting killer (apoptosis-inducing)
1456937	1.4730662 oviductal glycoprotein 1, 120kD (mucin 9, oviductin)
25274	1.464238 g20 protein
795288	1.4625618 ubiquitin specific protease 4 (proto-oncogene)
1569418	1.4599089 Homo sapiens cDNA FLJ11385 fis, clone HEMBA1000520
753700	1.4522717 Ras-related GTP-binding protein
1691237	1.4516493 ESTs
741891	1.450795 RAB2, member RAS oncogene family-like
1493383	1.4468163 Homo sapiens mRNA; cDNA DKFZp434H2418 (from clone DKFZp434H2418)
1675273	1.445145 RAR-related orphan receptor C
293916	1.4265341 FKBP-associated protein
39600	1.4224626 adenylate kinase 5
1573087	1.4200341 KIAA0592 protein
839796	1.4114662 candidate tumor suppressor p33 ING1 homolog
296123	1.4057088 Homo sapiens PRO1851 mRNA, complete cds
727263	1.4046408 heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)
265045	1.4041143 Homo sapiens mRNA; cDNA DKFZp586B0918 (from clone DKFZp586B0918)
869450	1.4034983 ribosomal protein L11
714472	1.4006155 KIAA0397 gene product

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825296	1.3963737	low density lipoprotein receptor defect C complementing
753301	1.3962897	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)
700527	1.394937	glutaredoxin (thioltransferase)
811565	1.3909974	KIAA1694 protein
1630990	1.3843882	ribosomal protein L29
70749	1.3810753	Homo sapiens cDNA: FLJ21874 fis, clone HEP02488
814826	1.3785178	ESTs
175103	1.376581	cadherin, EGF LAG seven-pass G-type receptor 2, flamingo (Drosophila) homolog
215000	1.3677098	vasoactive intestinal peptide receptor 1
810331	1.3656069	quiescin Q6
1681421	1.3645145	EGF-like-domain, multiple 3
502198	1.3619124	protein phosphatase 1, regulatory (inhibitor) subunit 5
825365	1.361275	hypothetical protein FLJ21919
1557047	1.3582677	thrombospondin 3
2067500	1.3579293	Z-band alternatively spliced PDZ-motif
490615	1.3566637	tubulin, gamma 2
743880	1.3528093	KIAA0263 gene product
812099	1.3444147	RNA binding motif protein 5
868652	1.3432331	complement component 4B
120138	1.3384804	J domain containing protein 1
156363	1.3358314	hypothetical protein FLJ12934
813584	1.3327194	p53 regulated PA26 nuclear protein
726703	1.3247883	Homo sapiens clone 23736 mRNA sequence
809507	1.3225829	hypothetical protein FLJ20568
2018423	1.3212314	death-associated protein kinase 2
292806	1.3201283	chromosome segregation 1 (yeast homolog)-like
741977	1.3200635	B-factor, properdin
610326	-4.5776738	
322494	-3.6341126	core-binding factor, beta subunit
824962	-3.6328144	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
825659	-3.6247426	N-myc downstream regulated
796694	-3.5038212	baculoviral IAP repeat-containing 5 (survivin)

- 149355 -3.4959791 translocating chain-associating membrane protein
- 814270 -3.3246381 polymyositis/scleroderma autoantigen 1 (75kD)
- 884425 -3.3113482 chaperonin containing TCP1, subunit 5 (epsilon)
- 1874367 -3.2390912 small inducible cytokine subfamily A (Cys-Cys), member 20
- 742707 -3.2093502 ESTs, Weakly similar to MUC2_HUMAN MUCIN 2
PRECURSOR [H.sapiens]
- 321354 -3.1386611 mitochondrial ribosomal protein L15
- 280375 -3.110486 PRO2000 protein
- 2018154 -3.0906181 electron-transfer-flavoprotein, beta polypeptide
- 814792 -3.0561472 ubiquitin specific protease 10
- 826070 -3.0517117 KIAA0948 protein
- 624867 -2.9688171 hypothetical protein FLJ20186
- 202035 -2.9361687 uncharacterized hypothalamus protein HT010
- 1476053 -2.9129535 RAD51 (S. cerevisiae) homolog (E coli RecA homolog)
- 194318 -2.8913426 hypothetical protein MGC5585
- 769921 -2.8415969 ubiquitin carrier protein E2-C
- 1732922 -2.8216808 Homo sapiens mRNA; cDNA DKFZp762H106 (from clone
DKFZp762H106)
- 1536236 -2.7995652 hypothetical protein FLJ13154
- 200402 -2.7793137 hypothetical protein dJ616B8.3
- 815556 -2.7693 hypothetical protein FLJ10430
- 1055607 -2.7538365 SUMO-1 activating enzyme subunit 1
- 1466621 -2.7448687 ATPase, Ca++ transporting, type 2C, member 1
- 770675 -2.6929924 Homo sapiens cDNA: FLJ21323 fis, clone COL02374
- 79520 -2.6909833 RAB2, member RAS oncogene family
- 950355 -2.6845343 ESTs, Weakly similar to S13495 pregnancy zone protein
[H.sapiens]
- 79710 -2.6813265 KIAA0174 gene product
- 2011138 -2.6569485 KIAA1036 protein
- 898333 -2.6509707 ESTs
- 878846 -2.6361347 brain protein I3
- 842818 -2.63282 lysyl-tRNA synthetase
- 1553065 -2.627227 hypothetical protein FLJ14993

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136722 -2.6269431 ATPase, Na⁺/K⁺ transporting, beta 3 polypeptide

308633 -2.6261051 hypothetical protein FLJ10339

854581 -2.6159344 transcription factor 4

951241 -2.5987959 clone HQ0310 PRO0310p1

292936 -2.5940369 hypothetical protein FLJ10468

781047 -2.569753 budding uninhibited by benzimidazoles 1 (yeast homolog)

823907 -2.5587562 hypothetical protein FLJ10511

377368 -2.5495557 cell death regulator aven

292388 -2.5448438

122241 -2.539248 proteasome (prosome, macropain) subunit, beta type, 2

731223 -2.5364769 proteasome (prosome, macropain) subunit, beta type, 2

1660666 -2.534682 carbonic anhydrase VB, mitochondrial

825470 -2.530053 topoisomerase (DNA) II alpha (170kD)

1472719 -2.526978 SMT3 (suppressor of mif two 3, yeast) homolog 1

869375 -2.5249164 isocitrate dehydrogenase 2 (NADP⁺), mitochondrial

302292 -2.5097213 exostoses (multiple) 2

1175007 -2.4998247 tumor necrosis factor receptor superfamily, member 10d,
decoy with truncated death domain

1422338 -2.488461 ribonucleotide reductase M2 polypeptide

2014034 -2.4843808 methylene tetrahydrofolate dehydrogenase (NAD⁺
dependent), methenyltetrahydrofolate cyclohydrolase

50884 -2.4377483 dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2

1474424 -2.4345879 Homo sapiens cDNA FLJ12758 fis, clone NT2RP2001328

753285 -2.4324065 glycogenin

700792 -2.4311609 cyclin-dependent kinase inhibitor 3 (CDK2-associated dual
specificity phosphatase)

259950 -2.4310983 hypothetical protein FLJ14991

610326 -2.4214624

284004 -2.4185183 ESTs

756595 -2.3963227 S100 calcium-binding protein A10 (annexin II ligand, calpactin
I, light polypeptide (p11))

128711	-2.3891503	anillin (Drosophila Scraps homolog), actin binding protein
1582738	-2.3882015	uncharacterized bone marrow protein BM040
1915867	-2.3829702	Homo sapiens cDNA: FLJ21086 fis, clone CAS03272
754582	-2.3765311	ecotropic viral integration site 2A
462961	-2.3685047	dihydrofolate reductase
705064	-2.3682586	transforming, acidic coiled-coil containing protein 3
1553696	-2.3605995	vanin 1
129294	-2.3507956	ESTs
809588	-2.3342142	gamma-glutamyl hydrolase (conjugase, folypolygammaglutamyl hydrolase)
1909526	-2.333814	ESTs, Weakly similar to 2004399A chromosomal protein [H.sapiens]
815771	-2.3166739	chromosome 7 open reading frame 2
703707	-2.2865473	aspartate beta-hydroxylase
2017415	-2.2832169	centromere protein A (17kD)
1650942	-2.2797717	Human proteinase activated receptor-2 mRNA, 3'UTR
645079	-2.2761946	3'(2'), 5'-bisphosphate nucleotidase 1
133213	-2.2753496	fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)
788566	-2.2752004	Purkinje cell protein 4
2009574	-2.2646007	T brachyury (mouse) homolog
1897302	-2.2563379	serine/threonine kinase 17b (apoptosis-inducing)
78869	-2.2539078	cell membrane glycoprotein, 110000M(r) (surface antigen)
590759	-2.2513499	sterol-C4-methyl oxidase-like
785368	-2.2489394	PDZ-binding kinase; T-cell originated protein kinase
1714689	-2.2489064	ESTs
795197	-2.2481741	ubiquitin-conjugating enzyme E2E 2 (homologous to yeast UBC4/5)
781472	-2.2390098	Tax1 (human T-cell leukemia virus type I) binding protein 1
1469966	-2.2375228	delta (Drosophila)-like 3
1587847	-2.2354975	minichromosome maintenance deficient (mis5, S. pombe) 6
209066	-2.2325695	
1035796	-2.2308926	ESTs

sd-71385

sd-71385

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1517595 -2.0965219 KIAA0175 gene product
282428 -2.0954489 ESTs, Weakly similar to A46010 X-linked retinopathy protein
[H.sapiens]
1883219 -2.0949091 ESTs
746229 -2.0906355 mitogen-activated protein kinase kinase kinase kinase 4

610326 -2.0896786 hypothetical protein MGC12992
1632225 -2.0828168 ESTs
743810 -2.0796998 hypothetical protein MGC2577
1416055 -2.0725881 extra spindle poles, *S. cerevisiae*, homolog of

1626297 -2.0656173 hypothetical protein FLJ20509
852829 -2.0608067 karyopherin alpha 3 (importin alpha 4)
840511 -2.0554449 vimentin
278504 -2.0519206 neurochondrin
1534700 -2.0506628 KIAA0830 protein
812276 -2.0458249 synuclein, alpha (non A4 component of amyloid precursor)

306841 -2.0449642 T cell receptor beta locus
3172883 -2.0437672 ESTs, Weakly similar to 1709359A dopamine D4 receptor
[H.sapiens]
624627 -2.0409259 ribonucleotide reductase M2 polypeptide
486179 -2.0380168 Homo sapiens cDNA FLJ10205 fis, clone HEMBA1004954

376316 -2.0218598 wee1+ (*S. pombe*) homolog
37671 -2.0190035 hypothetical protein FLJ21610
629944 -2.0166696 myosin VB
713158 -2.0133834 ESTs
504308 -2.0067977 hypothetical protein FLJ10540
1605426 -1.9957389 hypothetical protein FLJ13352
810711 -1.9920785 stearyl-CoA desaturase (delta-9-desaturase)

263790 -1.9904129 isocitrate dehydrogenase 3 (NAD+) alpha
549349 -1.9893582 hypothetical protein PRO1068
109221 -1.9879196 KIAA0286 protein
51773 -1.9875155 hypothetical protein MGC3077

Example X: Crossvalidation

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The following table shows the results of crossvalidation analysis (as described in Example I above) of various pair-wise comparisons. The two members of the pairwise comparison are indicated as "Class 1" and "Class 2" with the number of samples analyzed indicated under "N". The number of genes used to predict is indicated, along with the accuracy (in percent) for each combination. "FP" and "FN" refer to "false positive" and "false negative", respectively, as incorrectly identified for each of the two classes.

Class 1		Class 2		Genes	Accuracy	Class 1		Class 2	
Name	N	Name	N			FP	FN	FP	FN
Normal	28	Abnormal	57	850	99	0	1	1	0
Normal	28	ADH	7	600	100	0	0	0	0
Normal	28	DCIS	28	1300	100	0	0	0	0
ADH	7	DCIS	28	350	97	0	1	1	0
ADH	7	DCIS	28	10	97	0	1	1	0
N+ADH	36	DCIS+IDC	49	400	98	1	1	1	1
DCIS-I	7	DCIS-III	9	300	100	0	0	0	0
IDC-I	4	IDC-III	8	300	100	0	0	0	0

References:

DeRisi, J., et al., *Use of a cDNA microarray to analyse gene expression patterns in human cancer*, Nature Genetics, (1996) 14:457-460.

Hedenfalk, I., et al., *Gene-Expression Profiles In Heredity Breast Cancer*, The New England Journal of Medicine, (February 22, 2001) 344:8:539-548.

Golub, T. R., et al., *Molecular Classification of Cancer: Class Discovery and Class Prediction by Gene Expression Monitoring*, Science, (October 15, 1999) 286:531-537.

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Perou, Charles M., et al., *Molecular portraits of human breast tumours*, Nature, (August 17, 2000) 406:747-752.

Garber, Mitchell E., et al., *Diversity of gene expression in adenocarcinoma of the lung*, Proc. Natl. Acad. Sci. USA, (November 20, 2001) 98:24:13784-13789.

Perou, Charles M., et al., *Distinctive gene expression patterns in human mammary epithelial cells and breast cancers*, Proc. Natl. Acad. Sci. USA, (August 1999) 96:9212-9217.

Sgrio, Dennis C., et al., *In Vivo Gene Expression Profile Analysis of Human Breast Cancer Progression*, Cancer Research, (November 15, 1999) 59:5656-5661.

Sorlie, Therese, et al., *Gene expression patterns of breast carcinomas distinguish tumor subclasses with clinical implications*, Proc. Natl. Acad. Sci., (September 11, 2001) 98:19:10869-10874.

Alizadeh, Ash A., et al., *Distinct types of diffuse large B-cell lymphoma identified by gene expression profiling*, Nature, (February 3, 2000) 403:503-511.

Bittner, M., et al., *Molecular classification of cutaneous malignant melanoma by gene expression profiling*, Nature (August 3, 2000) 406:536-540.

West, Mike, et al., *Predicting the clinical status of human breast cancer by using gene expression profiles*, Proc. Natl. Acad. Sci., (September 25, 2001) 98:20:11462-11467.

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All references cited herein, including patents, patent applications, and publications, are hereby incorporated by reference in their entireties, whether previously specifically incorporated or not.

Having now fully described this invention, it will be appreciated by those skilled in the art that the same can be performed within a wide range of equivalent parameters, concentrations, and conditions without departing from the spirit and scope of the invention and without undue experimentation.

While this invention has been described in connection with specific embodiments thereof, it will be understood that it is capable of further modifications. This application is intended to cover any variations, uses, or adaptations of the invention following, in general, the principles of the invention and including such departures from the present disclosure as come within known or customary practice within the art to which the invention pertains and as may be applied to the essential features hereinbefore set forth.

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